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(54) Title: COMPOSITIONS ISOLATED FROM FORAGE GRASSES AND METHODS FOR THEIR USE

(57) Abstract: Isolated polynucleotides encoding polypeptides active in the fructan, cellulose, starch and/or tannin biosynthetic pathways are provided, together with expression vectors and host cells comprising such isolated polynucleotides. Methods for the use of such polynucleotides and polypeptides are also provided.

COMPOSITIONS ISOLATED FROM FORAGE GRASSES AND METHODS FOR THEIR USE

Technical Field of the Invention

This invention relates to polynucleotides isolated from forage grass tissues, specifically from *Lolium perenne* (perennial ryegrass) and *Festuca arundinacea* (tall fescue), as well as oligonucleotide probes and primers, genetic constructs comprising the polynucleotides, biological materials (including host cells and plants) incorporating the polynucleotides, polypeptides encoded by the polynucleotides, and methods for using the polynucleotides and polypeptides. More particularly, the invention relates to polypeptides involved in the tannin, cellulose and fructan biosynthetic pathways, and to polynucleotides encoding such polypeptides.

Background of the Invention

Over the past 50 years, there have been substantial improvements in the genetic production potential of ruminant animals (sheep, cattle and deer). Levels of meat, milk or fiber production that equal an animal's genetic potential may be attained within controlled feeding systems, where animals are fully fed with energy dense, conserved forages and grains. However, the majority of temperate farming systems worldwide rely on the *in situ* grazing of pastures. Nutritional constraints associated with temperate pastures can prevent the full expression of an animal's genetic potential. This is illustrated by a comparison between milk production by North American grain-fed dairy cows and New Zealand pasture-fed cattle. North American dairy cattle produce, on average, twice the milk volume of New Zealand cattle, yet the genetic base is similar within both systems (New Zealand Dairy Board and United States Department of Agriculture figures). Significant potential therefore exists to improve the efficiency of conversion of pasture nutrients to animal products through the correction of nutritional constraints associated with pastures.

Carbohydrate metabolism

Plant carbohydrates can be divided into two groups depending on their function

within the plant. Structural carbohydrates, such as cellulose and lignin, are usually part of the extracellular matrix. Non-structural, storage carbohydrates act as either long- or short-term carbohydrate stores. Examples of non-structural carbohydrates include starch, sucrose and fructans.

Fructans are polymers that are stored in the vacuole and that consist of linear and branched chains of fructose units (for review see Vijn and Smeekens *Plant Physiol.* 120:351-359, 199). They play an important role in assimilate partitioning and possibly in stress tolerance in many plant families. Grasses use fructans instead of starch as a water-soluble carbohydrate store (Pollock *et al.*, in "Regulation of primary metabolic pathways in plants", N.J. Kruger *et al.* (eds), Kluwer Academic Publishers, The Netherlands, pp195-226, 1999). Increasing the amount of fructans and sucrose in forage crops leads to an increase in the level of water-soluble carbohydrates and thereby enhances the nutritional value of the plants. In addition, increasing the amount of fructans in forage plants decreases methane production in animals fed the plants, thereby leading to lower greenhouse gas emissions, and decreases urea production in animals as less protein is degraded in the rumen (Biggs and Hancock *Trends in Plant Sci.*, 6:8-9, 2001). Fructans have also been implicated in protecting plants against water deficits caused by drought or low temperatures. Introduction of enzymes involved in the fructan biosynthetic pathway into plants that do not naturally synthesize fructans may be employed to confer cold tolerance and drought tolerance (Pilon-Smits, *Plant Physiol.* 107:125-130, 1995).

The number of fructose units within a fructan chain is referred to as the degree of polymerization (DP). In grasses, fructans of DP 6-10 are common. Such fructans of low DP are naturally sweet and are therefore of interest for use as sweeteners in foodstuffs. Long fructan chains form emulsions with a fat-like texture and a neutral taste. The human digestive system is unable to degrade fructans, and fructans of high DP may therefore be used as low-calorie food ingredients. Over-expression of enzymes involved in the fructan biosynthetic pathway may be usefully employed to produce quantities of fructans that can be purified for human consumption.

Five major classes of structurally different fructans have been identified in plants, with each class showing a different linkage of the fructosyl residues. Fructans found in grasses are of the mixed levan class, consisting of both (2-1)- and (2-6)-linked beta-D-

fructosyl units (Pollock *et al.*, in "Regulation of primary metabolic pathways in plants", N.J. Kruger *et al.* (eds), Kluwer Academic Publishers, The Netherlands, pp195-226, 1999). Fructans are synthesized by the action of fructosyltransferase enzymes on sucrose in the vacuole. These enzymes are closely related to invertases, enzymes that normally hydrolyze sucrose.

Grasses use two fructosyltransferase enzymes to synthesize fructans, namely sucrose:sucrose 1-fructosyltransferase (1-SST) and sucrose:fructan 6-fructosyltransferase (6-SFT) (Pollock *et al.*, in "Regulation of primary metabolic pathways in plants", N.J. Kruger *et al.* (eds), Kluwer Academic Publishers, The Netherlands, pp195-226, 1999). 1-SST is a key enzyme in plant fructan biosynthesis, while 6-SFT catalyzes the formation and extension of beta-2,6-linked fructans that is typically found in grasses. Specifically, 1-SST catalyzes the formation of 1-kestose plus glucose from sucrose, while 6-SFT catalyzes the formation of bifurcose plus glucose from sucrose plus 1-kestose and also the formation of 6-kestose plus glucose from sucrose. Both enzymes can modify 1-kestose, 6-kestose and bifurcose further by adding additional fructose molecules. Over-expression of both 1-SST and 6-SFT in the same plant may be employed to produce fructans for use in human foodstuffs (Sevenier *et al.*, *Nature Biotechnology* 16:843-846; Hellewege *et al.*, *Proc. Nat. Acad. Sci., U.S.A.* 97:8699-8704). For a review of the fructan biosynthetic pathway see Vijn I. and Smeekens S. *Plant Physiol.* 120:351-359, 1999.

The synthesis of sucrose from photosynthetic assimilates in plants, and therefore the availability of sucrose for use in fructan formation, is controlled, in part, by the enzymes sucrose phosphate synthase (SPS) and sucrose phosphate phosphatase (SPP). Sucrose plays an important role in plant growth and development, and is a major end product of photosynthesis. It also functions as a primary transport sugar and in some cases as a direct or indirect regulator of gene expression (for review see Smeekens *Curr. Opin. Plant Biol.* 1:230-234, 1998). SPS regulates the synthesis of sucrose by regulating carbon partitioning in the leaves of plants and therefore plays a major role as a limiting factor in the export of photoassimilates out of the leaf. The activity of SPS is regulated by phosphorylation and moderated by concentration of metabolites and light (Huber *et al.*, *Plant Physiol.* 95:291-297, 1991). Specifically, SPS catalyzes the transfer of glucose from UDP-glucose to fructose-6-phosphate, thereby forming sucrose-6-phosphate (Suc-6-P). Suc-6-P is then

dephosphorylated by SPP to form sucrose (Lunn *et al., Proc. Nat. Acad. Sci., U.S.A.* 97:12914-12919, 2000). The enzymes SPS and SPP exist as a heterotetramer in the cytoplasm of mesophyll cells in leaves, with SPP functioning to regulate SPS activity. SPS is also important in ripening fruits, sprouting tubers and germinating seeds (Laporte *et al. Planta* 212:817-822, 2001).

Once in the vacuole, sucrose can be converted into fructan by fructosyltransferases as discussed above, or hydrolyzed into glucose and fructose by the hydrolase enzymes known as invertases (Sturm, *Plant Physiol.* 121:1-7, 1999). There are several different types of invertases, namely extracellular (cell wall), vacuolar (soluble acid) and cytoplasmic, with at least two isoforms of each type of invertase normally being found within a plant species. In addition to having different subcellular locations, the different types of invertases have different biochemical properties. For example, soluble and cell wall invertases operate at acidic pH, whereas cytoplasmic invertases work at a more neutral or alkaline pH. Invertases are believed to regulate the entry of sucrose into different utilization pathways (Grof and Campbell *Aust. J. Plant Physiol.* 28:1-12, 2001). Reduced invertase activity may increase the level of water-soluble carbohydrates in plants. Plants contain several isoforms of cell wall invertases (CWINV), which accumulate as soluble proteins. CWINV plays an important role in phloem unloading and in stress response. *Arabidopsis* contains 9 putative cytoplasmic or neutral invertases that are expressed in all tissues and at all developmental stages implying a more general function than the differentially expressed acid invertases. The neutral invertase cloned from carrot and *Lolium temulentum* show no similarity to acid invertases with the exception of a conserved pentapeptide motif in the grass cDNA (Gallagher *J. Exp. Bot.* 49:789, 1998; Sturm, A. et al., *Physiologia Plantarum*, 107:159-265, 1999).

Another enzyme that acts upon sucrose in plants is soluble sucrose synthase (SUS). Recent results indicate that SUS is localized in the cytosol, associated with the plasma membrane and the actin cytoskeleton. Phosphorylation of SUS is one of the factors controlling localization of the enzyme (Winter and Huber, *Crit. Rev. Biochem. Mol. Biol.* 35:253-89, 2000). It catalyzes the transfer of glucose from sucrose to UDP, yielding UDP-glucose and fructose. Increasing the amount of SUS in a plant increases the amount of cellulose synthesis, whereas decreasing SUS activity should increase fructan levels. Increased SUS concentration may also increase the yield of fruiting bodies. SUS activity is

highest in carbon sink tissues in plants and low in photosynthetic source tissues, and studies have indicated that SUS is the main sucrose-cleaving activity in sink tissues. Grasses have two isoforms of SUS that are encoded by separate genes. These genes are differentially expressed in different tissues.

Pyrophosphate-fructose 6-phosphate 1-phosphotransferase (PFP, EC 2.7.1.90) catalyses the reversible conversion of fructose 6-phosphate (Fru-6-P) and pyrophosphate (Pp_i) to fructose 1,6-bisphosphate (Fru-1,6-P) and inorganic phosphate (P_i). In the plant PFP has important physiological roles in glycosylation, sucrose metabolism, respiratory carbon flow, as well as being a supply of PP_i. Along with FBPase and PFK, PFP regulates this step in the pathway of sucrose metabolism. PFP is a cytoplasmic enzyme consisting of a 250kDa tetramer (two alpha and two beta chains) with the two subunits containing all of the regulatory and catalytical functions, respectively. In the plant cell fructose 2-6-bisphosphate is a potent activator of PFP activity. In sugarcane (a C_4 grass), PFP activity is inversely correlated with sucrose content (Whittaker and Botha *Plant Physiol.*, 115, 1651-1659, 1997), indicating that a reduction of PFP enzyme levels will increase the flux of sucrose synthesis. In forage grasses reducing PFP levels in the leaves will increase water-soluble carbohydrate levels in the leaf tissue. The *Arabidopsis* genome contains four closely related PFP genes thought to encode two isoforms of each subunit, however, only 1 cDNA representing each unit of the purified protein has been isolated from Castor Bean, Potato and Spinach (Todd, Blakeley and Dennis *Gene*, 152, 181-186, 1995; Carlisle, Blakeley, Hemmingsen, Trevanion, Hiyoshi, Kruger and Dennis *J. Biol. Chem.*, 265, 18366-18371, 1990).

Sucrose Transporters (SUTs) play a major role in the partitioning of dissacharides (sucrose) across membranes (for a review see Williams et al., *Trends Plant Sci.*, 5:283-290, 2000). In particular SUTs are involved in loading and unloading of sucrose into the phloem and the source-sink relationship within the plant. SUTs are energy depenedent and can transport sucrose across large sucrose gradients. In *Arabidopsis* six SUTs have been identified, however in monocots and dicots SUTs form distinct groups. In general, monocots have 2 types of SUTs. For example barley and maize have two SUT proteins, known as SUT1 and SUT2. SUT1 is found in source, not sink, tissues, whereas SUT2 is constitutively expressed at similar levels in all tissues (Hirose, Imaizumi, Scofield, Furbank and Ohsugi *Plant Cell Physiol.* 38: 1389-1396; 1997; Weschke, et al., *Plant Journal* 21, 455-457, 2000).

Inhibition of SUT1 in potato plants by antisense technology resulted in increased levels of sucrose and starch in the source leaves (Schulz et al. *Planta*, 206, 533-543, 1998). Repressing SUT activity in forage grasses to lower phloem loading in source tissues will increase water soluble carbohydrate content in the leaves.

Cellulose synthesis

The major source of dietary fibre for grazing animals comes from plant cell walls. Mammals possess no enzymes capable for breaking down the polysaccharides in plant cell walls. Instead animals such as ruminants depend on microbial breakdown of plant cell walls through fermentation in either the rumen or large intestine.

Fibre in plants is measured using the Neutral Detergent Fibre (NDF) technique in which plant samples are boiled in a solution containing sodium lauryl sulfate (van Soest *in* "Nutritional Ecology of the Ruminant". Cornell University Press, Ithaca, NY, 1994). This detergent extracts water-soluble components such as sugars, lipids and organic acids. The remaining insoluble residue (fibre) is termed NDF and consists predominantly of plant cell wall components such as cellulose, hemicellulose, and lignin. The amount of cellulose and lignin in cell walls can be determined using the Acid Detergent Fibre (ADF) method where plant samples are boiled in sulfuric acid and sodium lauryl sulfate. The difference between NDF and ADF for a plant sample is normally considered to be the amount of hemicellulose (van Soest *in* "Nutritional Ecology of the Ruminant". Cornell University Press, Ithaca, NY, 1994).

Stems of most forage species have greater NDF content then leaves. For example, for a temperate C_3 grass in mid-flowering such as tall fescue (*Festuca arundinacea*), NDF content of leaves and stems is 50 and 70%, respectively (Buxton & Redfearn *J. Nutrition* 127:S814-S818, 1997). In contrast, for a C_4 tropical grass such as switchgrass (*Panicum virgatum* L.) the NDF content of leaves and stems is 70 and 85%, respectively. The digestibility of a forage is determined by cell wall content, so that legumes are more digestible than grasses because they contain less NDF. The NDF of a legume, however, is generally less digestible than that of grasses because a higher proportion of the NDF is made up by lignin. The increase of lignin as a component of NDF is also responsible for the decrease in digestibility of grasses at the time of flowering. In fact, ruminants can digest

only 40-50% of NDF in legumes compared to 60-70% for grass NDF (Buxton & Redfearn *J. Nutrition* 127:S814-S818, 1997). Digestibility of cellulose by ruminants is therefore directly related to the extent of lignification. Generally hemicellulose is more digestible than cellulose.

Cellulose is the most abundant carbohydrate in forage making up to 20-40% of dry matter (van Soest *in* "Nutritional Ecology of the Ruminant". Cornell University Press, Ithaca, NY, 1994). The cellulose in forages consists predominantly of β1-4 glucan (85%) and smaller amounts of pentosans (e.g. xylose and arabinose; 15%). There appear to be two pools of cellulose within the plant cell wall, the difference being one is lignified and the other is not (van Soest *in* "Nutritional Ecology of the Ruminant". Cornell University Press, Ithaca, NY, 1994). The lignified cellulose is mostly found in the primary cell wall and in the S1 outer layer of the secondary cell wall. Independent of lignification, it appears that cellulose possesses a variability in nutritive quality (van Soest *in* "Nutritional Ecology of the Ruminant". Cornell University Press, Ithaca, NY, 1994). This indicates that it is possible to alter the rate of cellulose digestibility by modifying the chemical composition of cellulose. This could be achieved through manipulating the actions of the cellulose synthesis and cellulose synthesis-like enzymes found in plant cells. One method to increase digestibility in this way is to increase the activity of the cellulose synthesis and cellulose synthesis-like enzymes responsible for synthesizing hemicellulose or to down regulate the cellulose synthesis and cellulose synthesis-like enzymes making cellulose. Hemicellulose is much more digestible than cellulose and is less likely to become lignified. Another way of manipulating cell wall composition is through modifying the rate and supply of primary components required for cellulose synthesis, i.e. of β1-4 glucan and pentosans such as xylose and arabinose. One way to achieve this is to modify the actions of soluble sucrose synthase and UDP glucose pyrophophorylase (UDP-GP) enzymes that produce the UDP-glucose required for cellulose synthesis. This may be further modified by manipulating the actions of the large and small subunits of ADP-glucose pyrophosphorylase (ADP-GP), the two enzymes that are rate-limiting steps in starch synthesis (Smith, Denyer and Martin *Ann. Rev. Plant Phys. Plant Mol. Biol.* 48:67-87, 1997).

Manipulating expression of the UDPGP and ADP-GP genes would alter the chemical composition of plant cell walls in forage plants. Altering cell wall biosynthesis therefore provides an opportunity to increase digestibility of the plant dry matter. This may be achieved by increasing the amount of carbon in the plant allocated to cellulose biosynthesis at the expense of lignin biosynthesis. Alternatively, decreasing the amount of cellulose biosynthesis and increasing the amount of water-soluble carbohydrates would have a similar effect. Furthermore, specifically increasing hemicellulose levels in the plant cell walls at expense of cellulose would also increase forage digestibility. By utilizing specific promoters in combination with the UDPGP and ADP-GP genes it is possible to increase or decrease the starch, cellulose and/or hemicellulose levels in the leaf or stem.

Tannin Biosynthetic Pathway

Condensed tannins are polymerized flavonoids. More specifically, tannins are composed of catechin 4-ol and catechin monomer units, and are stored in the vacuole. In many temperate forage crops, such as ryegrass and fescue, foliar tissues are tannin-negative. This leads to a high initial rate of fermentation when these crops are consumed by ruminant livestock resulting in both protein degradation and production of ammonia by the livestock. These effects can be reduced by the presence of low to moderate levels of tannin. In certain other plant species, the presence of high levels of tannins reduces palatability and nutritive value. Introduction of genes encoding enzymes involved in the biosynthesis of condensed tannins into a plant may be employed to synthesize flavonoid compounds that are not normally made in the plant. These compounds may then be isolated and used for treating human or animal disorders or as food additives.

Much of the biosynthetic pathway for condensed tannins is shared with that for anthocyanins, which are pigments responsible for flower color. Therefore, modulation of the levels of enzymes involved in the tannin biosynthetic pathway may be employed to alter the color of foliage and the pigments produced in flowers.

Most tannins described to date contain pro-cyanidin units derived from dihydroquercetin and pro-delphinidin units derived from dihydromyricetin. However, some tannins contain pro-pelargonidin units derived from dihydrokaempferol. The initial step in the tannin biosynthetic pathway is the condensation of coumaryl CoA with malonyl CoA to

give naringenin-chalcone, which is catalyzed by the enzyme chalcone synthase (CHS). The enzyme chalcone isomerase (CHI) catalyzes the isomerization of naringenin chalcone to naringenin (also known as flavanone), which is then hydroxylated by the action of the enzyme flavonone 3- beta-hydroxylase (F3βH) to give dihydrokaempferol. The enzyme flavonoid 3'-hydroxylase (F3'OH) catalyzes the conversion of dihydrokaempferol to dihydroquercetin, which in turn can be converted into dihydromyricetin by the action of flavonoid 3'5'-hydroxylase (F3'5'OH). F3'OH is a P450 enzyme responsible for the brick red to orange pelargonidin-based pigments, whereas F3'5'OH is responsible for the purple and blue delphinidin-based pigments. The enzyme dihydroflavonol-4-reductase (DFR) catalyzes the last step before dihydrokaempferol, dihydroquercetin and dihydromyricetin are committed for either anthocyanin (flower pigment) or proanthocyanidin (condensed tannin) formation. DFR also converts dihydrokaempferol to afzelchin-4-ol, dihydroquercetin to catechin-4-ol, and dihydromyricetin to gallocatechin-4-ol, probably by the action of more than one isoform. For a review of the tannin biosynthetic pathway, see, Robbins M.P. and Morris P. in Metabolic Engineering of Plant Secondary Metabolism, Verpoorte and Alfermann (eds), Kluwer Academic Publishers, the Netherlands, 2000. The leucoanthocyanidin dioxygenase (LDOX) enzyme belongs to the iron/ascorbate-dependent family of oxidoreductases. In maize the LDOX gene A2 is required for the oxidation of leucoanthocyanidins into anthocyanidins (Menssen, Hoehmann, Martin, Schnable, Peterson, Saedler and Gierl *EMBO J.* 9:3051-3057, 1990).

While polynucleotides encoding some of the enzymes involved in the fructan, cellulose and tannin biosynthetic pathways have been isolated for certain species of plants, genes encoding many of the enzymes in a wide range of plant species have not yet been identified. Thus there remains a need in the art for materials useful in the modification of fructan and tannin content and composition in plants, and for methods for their use.

Summary of the Invention

The present invention provides enzymes involved in the fructan, cellulose, starch and/or tannin biosynthetic pathways that are encoded by polynucleotides isolated from forage grass tissues. The polynucleotides were isolated from *Lolium perenne* (perennial ryegrass)

and *Festuca arundinacea* (tall fescue) tissues taken at different times of the year, specifically in winter and spring, and from different parts of the plants, including: leaf blades, leaf base, pseudostems, roots and stems. Genetic constructs, expression vectors and host cells comprising the inventive polynucleotides are also provided, together with methods for using the inventive polynucleotides and genetic constructs to modulate the biosynthesis of fructans and tannins.

In specific embodiments, the isolated polynucleotides of the present invention comprise a sequence selected from the group consisting of: (a) SEQ ID NO: 1-44; (b) complements of SEQ ID NO: 1-44; (c) reverse complements of SEQ ID NO: 1-44; (d) reverse sequences of SEQ ID NO: 1-44; (e) sequences having a 99% probability of being functionally or evolutionarily related to a sequence of (a)-(d), determined as described below; and (f) sequences having at least 75%, 80%, 90%, 95% or 98% identity to a sequence of (a)-(d), the percentage identity being determined as described below. Polynucleotides comprising at least a specified number of contiguous residues ("*x*-mers") of any of SEQ ID NO: 1-44, and oligonucleotide probes and primers corresponding to SEQ ID NO: 1-44 are also provided. All of the above polynucleotides are referred to herein as "polynucleotides of the present invention."

In further aspects, the present invention provides isolated polypeptides encoded by the inventive polynucleotides. In specific embodiments, such polypeptides comprise an amino acid sequence of SEQ ID NO: 45-88. The present invention also provides polypeptides comprising a sequence having at least 75%, 80%, 90%, 95% or 98% identity to a sequence of SEQ ID NO: 45-88, wherein the polypeptide possesses the same functional activity as the polypeptide comprising a sequence of SEQ ID NO: 45-88. The present invention also contemplates isolated polypeptides comprising at least a functional portion of an amino acid sequence selected from the group consisting of: (a) SEQ ID NO: 45-88; and (b) sequences having at least 75%, 80%, 90%, 95% or 98% identity to a sequence of SEQ ID NO: 45-88.

In another aspect, the present invention provides genetic constructs, or expression vectors, comprising a polynucleotide of the present invention, either alone, in combination with one or more of the inventive sequences, or in combination with one or more known polynucleotides.

In certain embodiments, the present invention provides genetic constructs comprising, in the 5'-3' direction: a gene promoter sequence; an open reading frame coding for at least a functional portion of a polypeptide of the present invention; and a gene termination sequence. An open reading frame may be orientated in either a sense or anti-sense direction. Genetic constructs comprising a non-coding region of a polynucleotide of the present invention or a polynucleotide complementary to a non-coding region, together with a gene promoter sequence and a gene termination sequence, are also provided. Preferably, the gene promoter and termination sequences are functional in a host cell, such as a plant cell. Most preferably, the gene promoter and termination sequences are those of the original enzyme genes but others generally used in the art, such as the Cauliflower Mosaic Virus (CMV) promoter, with or without enhancers, such as the Kozak sequence or Omega enhancer, and the *Agrobacterium tumefaciens* nopalin synthase terminator may be usefully employed in the present invention. Tissue-specific promoters may be employed in order to target expression to one or more desired tissues. The construct may further include a marker for the identification of transformed cells.

In a further aspect, transgenic cells, such as transgenic plant cells, comprising the genetic constructs of the present invention are provided, together with tissues and plants comprising such transgenic cells, and fruits, seeds and other products, derivatives, or progeny of such plants.

In yet another aspect, the present invention provides methods for modulating the fructan, cellulose, starch and/or tannin content and composition of a target organism, such as a plant, by modulating the amount and/or activity of an inventive polynucleotide or polypeptide in the organism. In certain embodiments, such methods include stably incorporating into the genome of the target plant a genetic construct of the present invention. In a preferred embodiment, the target plant is a forage grass, preferably selected from the group consisting of *Lolium* and *Festuca* species, and most preferably from the group consisting of *Lolium perenne* and *Festuca arundinacea*.

In a related aspect, methods for producing a plant having altered fructan or tannin composition is provided. Such methods comprise modulating the amount and/or activity of an inventive polynucleotide or polypeptide in a plant cell by, for example, transforming a plant cell with a genetic construct of the present invention to provide a transgenic cell, and

cultivating the transgenic cell under conditions conducive to regeneration and mature plant growth.

In yet a further aspect, the present invention provides methods for modifying the activity of an enzyme in a target organism, such as a plant, comprising modulating the amount and/or activity of an inventive polynucleotide or polypeptide in the target organism by, for example stably incorporating into the genome of the target organism a genetic construct of the present invention. In a preferred embodiment, the target plant is a forage grass, preferably selected from the group consisting of *Lolium* and *Festuca* species, and most preferably from the group consisting of *Lolium perenne* and *Festuca arundinacea*.

Brief Description of the Figures

Fig. 1 shows the neutral invertase activity of the recombinant grass alkaline/neutral invertase protein AN_INV8 from *L. perenne* (amino acid sequence provided in SEQ ID NO: 56; cDNA sequence provided in SEQ ID NO: 12). Activity was measured as the µg of glucose release from cleavage of sucrose per hour at pH 7. Also shown is an empty vector negative control (pET41a).

Fig. 2 shows the PFP activity of *L. perenne* and *F. arundinacea* PFPA and PFPB subunits in coupled reactions. Amino acid sequences for *L. perenne* PFPA and PFPB are given in SEQ ID NO: 59 and 62, respectively (corresponding cDNA sequences are SEQ ID NO: 15 and 18), and amino acid sequences for *F. arundinacea* PFPA and PFPB are given in SEQ ID NO: 60 and 63, respectively (corresponding cDNA sequences are SEQ ID NO: 16 and 19). Oxidation of NADH was measured as nmoles PPi converted.

Fig. 3 shows the amino acid sequence of SEQ ID NO: 45. The conserved UTP-glucose-1-phosphate uridylyltransferase domain is underlined.

Fig. 4 shows the amino acid sequence of SEQ ID NO: 46. The conserved UTP--glucose-1-phosphate uridylyltransferase domain is underlined.

Fig. 5 shows the amino acid sequence of SEQ ID NO: 47. The conserved glycoside hydrolase, family 32 domain is underlined.

Fig. 6 shows the amino acid sequence of SEQ ID NO: 48. A transmembrane domain is underlined.

Fig. 7 shows the amino acid sequence of SEQ ID NO: 53. The signal peptide is in bold/italics.

Fig. 8 shows the amino acid sequence of SEQ ID NO: 54. The signal peptide is in bold/italics and two conserved Antifreeze protein, type I domains are underlined.

Fig. 9 shows the amino acid sequence of SEQ ID NO: 55. The signal peptide is in bold/italics.

Fig. 10 shows the amino acid sequence of SEQ ID NO: 56. Two transmembrane domains are double underlined.

Fig. 11 shows the amino acid sequence of SEQ ID NO: 57. Two transmembrane domains are double underlined.

Fig. 12 shows the amino acid sequence of SEQ ID NO: 58. Two transmembrane domains are double underlined.

Fig. 13 shows the amino acid sequence of SEQ ID NO: 59. The conserved phosphofructokinase domain is underlined and a transmembrane domain is double underlined.

Fig. 14 shows the amino acid sequence of SEQ ID NO: 60. The conserved phosphofructokinase domain is underlined and a transmembrane domain is double underlined.

Fig. 15 shows the amino acid sequence of SEQ ID NO: 61. The conserved phosphofructokinase is underlined.

Fig. 16 shows the amino acid sequence of SEQ ID NO: 62. The conserved phosphofructokinase domain is underlined.

Fig. 17 shows the amino acid sequence of SEQ ID NO: 63. The conserved phosphofructokinase domain is underlined.

Fig. 18 shows the amino acid sequence of SEQ ID NO: 64. The conserved glycosyl transferase, group 1 domain is underlined and two transmembrane domains are double underlined.

Fig. 19 shows the amino acid sequence of SEQ ID NO: 65. The conserved glycosyl transferase, group 1 domain is underlined and two transmembrane domains are double underlined.

Fig. 20 shows the amino acid sequence of SEQ ID NO: 66. The conserved substrate transporter domain is in bold and eleven transmembrane domains are double underlined.

Fig. 21 shows the amino acid sequence of SEQ ID NO: 67. Nine transmembrane domains are double underlined.

Fig. 22 shows the amino acid sequence of SEQ ID NO: 68. The conserved substrate transporter domain is in bold and eleven transmembrane domains are double underlined.

Fig. 23 shows the amino acid sequence of SEQ ID NO: 69. The conserved substrate transporter domain is in bold and eleven transmembrane domains are double underlined.

Fig. 24 shows the amino acid sequence of SEQ ID NO: 70. The conserved substrate transporter domain is in bold and eleven transmembrane domains are double underlined.

Fig. 25 shows the amino acid sequence of SEQ ID NO: 72. The conserved nucleotidyl transferase domain is in bold and three ADP-glucose pyrophosphorylase are boxed. Nine transmembrane domains are double underlined.

Fig. 26 shows the amino acid sequence of SEQ ID NO: 73. The conserved nucleotidyl transferase domain is in bold and three ADP-glucose pyrophosphorylase domains are boxed. A transmembrane domain is double underlined.

Fig. 27 shows the amino acid sequence of SEQ ID NO: 74. The conserved nucleotidyl transferase domain is in bold and three ADP-glucose pyrophosphorylase domains are boxed. A transmembrane domain is double underlined.

Fig. 28 shows the amino acid sequence of SEQ ID NO: 75. The conserved nucleotidyl transferase domain is in bold and three ADP-glucose pyrophosphorylase domains are boxed. The signal peptide is in bold/italics and a transmembrane domain is double underlined.

Fig. 29 shows the amino acid sequence of SEQ ID NO: 76. The conserved naringenin-chalcone synthase domain is underlined. The signal peptide is in bold/italics and a transmembrane domain is double underlined.

Fig. 30 shows the amino acid sequence of SEQ ID NO: 77. The conserved naringenin-chalcone synthase domain is underlined and two transmembrane domains are double underlined.

Fig. 31 shows the amino acid sequence of SEQ ID NO: 78. The conserved naringenin-chalcone synthase domain is underlined and two transmembrane domains are double underlined.

Fig. 32 shows the amino acid sequence of SEQ ID NO: 79. A transmembrane domain is double underlined.

Fig. 33 shows the amino acid sequence of SEQ ID NO: 80. A transmembrane domain is double underlined.

Fig. 34 shows the amino acid sequence of SEQ ID NO: 81. A transmembrane domain is double underlined.

Fig. 35 shows the amino acid sequence of SEQ ID NO: 82. The conserved Cytochrome P450 domain is underlined and three transmembrane domains are double underlined.

Fig. 36 shows the amino acid sequence of SEQ ID NO: 83. The conserved Cytochrome P450 domain is boxed, the signal peptide is in bold and a transmembrane domain is double underlined.

Fig. 37 shows the amino acid sequence of SEQ ID NO: 84. The conserved Cytochrome P450 domain is boxed and three transmembrane domains are double underlined.

Fig. 38 shows the amino acid sequence of SEQ ID NO: 85. The conserved Cytochrome P450 domain is boxed, the signal peptide is in bold/italics and three transmembrane domains are double underlined.

Fig. 39 shows the amino acid sequence of SEQ ID NO: 86. The conserved Cytochrome P450 domain is boxed and three transmembrane domains are double underlined.

Fig. 40 shows the amino acid sequence of SEQ ID NO: 87. The conserved Cytochrome P450 domain is boxed, the signal peptide is in bold/italics and three transmembrane domains are double underlined.

Fig. 41 shows the amino acid sequence of SEQ ID NO: 88. The conserved 2OG-Fe(II) oxygenase superfamily domain is underlined.

Detailed Description of the Invention

The polypeptides of the present invention, and the polynucleotides encoding such polypeptides, have activity in fructan, cellulose, starch and/or tannin biosynthetic pathways

in plants. Using the methods and materials of the present invention, the fructan, cellulose, starch and/or tannin content of a plant may be modulated by modulating expression of polynucleotides of the present invention, or by modifying the activity of the polynucleotides or polypeptides encoded by the polynucleotides. The isolated polynucleotides and polypeptides of the present invention may thus be usefully employed in the correction of nutritional imbalances associated with temperate pastures and to increase the yield of animal products from pastures.

The fructan, cellulose, starch and/or tannin content of a target organism, such as a plant, may be modified, for example, by incorporating additional copies of genes encoding enzymes involved in the fructan, cellulose, starch and/or tannin biosynthetic pathways into the genome of the target plant. Similarly, a modified fructan, cellulose, starch and/or tannin content can be obtained by transforming the target plant with anti-sense copies of such genes. In addition, the number of copies of genes encoding for different enzymes in the fructan, cellulose, starch and tannin biosynthetic pathways can be manipulated to modify the relative amount of each monomer unit synthesized, thereby leading to the formation of fructans, cellulose, starch or tannins having altered composition.

The present invention thus provides methods for modulating the polynucleotide and/or polypeptide content and composition of an organism. In certain embodiments, such methods involve stably incorporating into the genome of the organism a genetic construct comprising one or more polynucleotides of the present invention. In one embodiment, the target organism is a plant species, preferably a forage plant, more preferably a grass of the *Lolium* or *Festuca* species, and most preferably *Lolium perenne* or *Festuca arundinacea*. In related aspects, methods for producing a plant having an altered genotype or phenotype is provided, such methods comprising transforming a plant cell with a genetic construct of the present invention to provide a transgenic cell, and cultivating the transgenic cell under conditions conducive to regeneration and mature plant growth. Plants having an altered genotype or phenotype as a consequence of modulation of the level or content of a polynucleotide or polypeptide of the present invention compared to a wild-type organism, as well as components (seeds, etc.) of such plants, and the progeny of such plants, are contemplated by and encompassed within the present invention.

The isolated polynucleotides of the present invention additionally have utility in genome mapping, in physical mapping, and in positional cloning of genes. The polynucleotide sequences identified as SEQ ID NOS: 1-44 and their variants, may also be used to design oligonucleotide probes and primers. Oligonucleotide probes and primers have sequences that are substantially complementary to the polynucleotide of interest over a certain portion of the polynucleotide, preferably over substantially the entire length of the polynucleotides. Oligonucleotide probes designed using the inventive polynucleotides may be employed to detect the presence and examine the expression patterns of genes in any organism having sufficiently similar DNA and RNA sequences in their cells using techniques that are well known in the art, such as slot blot DNA hybridization techniques. Oligonucleotide primers designed using the polynucleotides of the present invention may be used for PCR amplifications. Oligonucleotide probes and primers designed using the inventive polynucleotides may also be used in connection with various microarray technologies, including the microarray technology of Affymetrix (Santa Clara, CA).

In a first aspect, the present invention provides isolated polynucleotide sequences identified in the attached Sequence Listing as SEQ ID NOS: 1-44, and polypeptide sequences identified in the attached Sequence Listing as SEQ ID NO: 45-88. The polynucleotides and polypeptides of the present invention have demonstrated similarity to the following polypeptides that are known to be involved in fructan, cellulose, starch and/or tannin biosynthetic processes:

TABLE 1

SEQ ID NO: DNA	SEQ ID NO: polypeptide	Category	Description
1, 2	45, 46	Carbohydrate metabolism	Homolog of UDP-glucose pyrophosphorylase (EC 2.7.7.9) (UDPGP or UGPASE) which is one of the key enzymes of the carbohydrate metabolic pathway. It plays a central role as glucosyl donor in cellular metabolic pathways. UDP-glucose pyrophosphorylase catalyzes the reversible uridylyl transfer from UDP-glucose to MgPPi, forming glucose 1-phosphate and MgUTP.
3, 4	47, 48	Fructan	Homolog of Sucrose (Suc):Suc 1-fructosyl-

SEQ ID NO: DNA	SEQ ID NO: polypeptide	Category	Description
		metabolism	transferase (1-SST) isolated from *L. perenne*. 1-SST is the key enzyme in plant fructan biosynthesis and catalyzes the *de novo* fructan synthesis from sucrose. Fructans play an important role in assimilation partitioning and in stress tolerance in many plants. It contains a typical signature of the glycosyl hydrolases family 32. The glycosyl hydrolases family 32 domain signature has a consensus of HYQPxxH/NxxNDPNG, where D is the active site residue (Henrissat, *Biochem. J.* 280:309-316, 1991).
5-14	49-58	Fructan metabolism	Homolog of alkaline/neutral invertase (AN-INV) that is involved in catalyzing sucrose into hexoses for utilization as a source of carbon and energy. AN-INV belongs to the family 32 of glycosyl hydrolases. Neutral invertase is an octamer of 456 kDa with subunits of 57 kDa, whereas alkaline invertase is a 504 kDa tetramer with subunits of 126 kDa. Neutral invertase also hydrolyzes raffinose and stachyose and, therefore, is a beta-fructo-furanosidase. In contrast, alkaline invertase is highly specific for sucrose (Lee and Sturm, *Plant Physi*ol. 112:1513-1522, 1996).
15, 16	59, 60	Fructan metabolism	Homologue of the alpha subunit of Pyro-phosphate-dependent 6-phosphofructo-1-phosphotransferase (PFPA) that plays a role in carbohydrate metabolism. PFP is involved in the first step of glycolysis in the phosphorylation of fructose 6-phosphate (Fru 6-P). PFPA acts as a regulatory protein in regulating both the catalytic activity and the Fru-2,6-P2-binding affinity of the beta subunit (Siebers *et al.*, *J. Bacteriol.* 180:2137-2143, 1998).
17-19	61-63	Fructan metabolism	Homolog of the beta subunit of Pyrophosphate-dependent 6-phosphofructo-1-phospho-transferase (PFPB) which plays a role in carbohydrate metabolism. PFP is involved in the first step of glycolysis in the phosphorylation of fructose 6-phosphate (Fru-6-P). The catalytic activity of the PFP enzyme is associated with the beta subunit PFPB while

SEQ ID NO: DNA	SEQ ID NO: polypeptide	Category	Description
			PFPA acts as a regulatory protein in regulating both the catalytic activity and the Fru-2,6-P2-binding affinity of the beta subunit (Carlisle *et al., J. Biol. Chem.* 265:18366-18371, 1990; Siebers *et al., J. Bacteriol.* 180:2137-2143, 1998).
20, 21	64, 65	Fructan metabolism	Homologue of sucrose phosphate synthase which is involved in the sucrose synthesis pathway. Sucrose plays an important role in plant growth and development and is a major end product of photosynthesis. It also functions as a primary transport sugar and in some cases as a direct or indirect regulator of gene expression. SPS-1 regulates the synthesis of sucrose by regulating carbon partitioning in the leaves of plants and therefore plays a major role as a limiting factor in the export of photoassimilates out of the leaf. The activity of SPS is regulated by phosphorylation and moderated by concentration of metabolites and light.
22-24	66-68	Fructan metabolism	Homologue of the sugar transporter SUT1, a member of the SUT family of low- and high-affinity sucrose transporters that is involved in transport of sucrose from mature leaves via the phloem. Expression of SUT1 has also been observed in other tissues (stems and parts of flower) suggesting that SUT1 may also have other functions, such as sucrose retrieval and phloem unloading (Burkle *et al., Plant Physi*ol. 118:59-68, 1998).
25, 26	69, 70	Fructan metabolism	Homologue of sugar transporter SUT2, a member of the SUT family of low- and high-affinity sucrose transporters. SUT2 is more highly expressed in sink than in source leaves, is inducible by sucrose and regulates the relative activity of low- and high-affinity sucrose transport into sieve elements (Barker *et al., Plant Cell* 12:1153-1164, 2000).
27	71	Fructan metabolism	Homologue of a sugar transporter, a member of the SUT family of low- and high-affinity sucrose transporters that is involved in transport of sucrose from mature leaves via the phloem.
28, 29	72, 73	Fructan	Homolog of the large subunit (LSU) of ADP-

SEQ ID NO: DNA	SEQ ID NO: polypeptide	Category	Description
		metabolism	glucose pyrophosphorylase (AGPase), which plays a role in starch biosynthesis. It catalyzes the synthesis of the activated glycosyl donor, ADP-glucose from glucose-1-phosphate and ATP. The enzyme is found in chloroplasts of leaves and amyloplasts of developing endosperm. AGPase belongs to the glucose-1-phosphate adenylyltransferase family.
30, 31	74, 75	Carbohydrate metabolism	Homolog of the small subunit (SSU) of ADP-glucose pyrophosphorylase (AGPase), which plays a role in starch biosynthesis. It catalyzes the synthesis of the activated glycosyl donor, ADP-glucose from glucose-1-phosphate and ATP. The enzyme is found in chloroplasts of leaves and amyloplasts of developing endosperm. AGPase belongs to the glucose-1-phosphate adenylyltransferase family.
32, 33	76, 77	Tannin biosynthesis	Homolog of Chalcone Synthase (CHS) which is an important enzyme in flavonoid synthesis.
34-37	78-81	Tannin metabolism	Homologue of dihydroflavonal-4-reductase (DFR) that belongs to the dihydroflavonol-4-reductases family and is involved in the flavonoid synthesis and anthocyanidins biosynthesis. Flavonoids are secondary metabolites derived from phenylalanine and acetate metabolism that perform a variety of essential functions in higher plants.
38-43	82-87	Tannin metabolism	Homologue of flavonoid 3'-hydroxylase (F3'H) which is a key enzyme in the flavonoid pathway leading to the production of the colored anthocyanins where it is involved in determination of flower coloring. Anthocyanins synthesized in plants are controlled by flavonoid 3'-hydroxylase and flavonoid 3',5'-hydroxylase which are members of the cytochrome P450 family, a large group of membrane-bound heme-containing enzymes that are involved in a range of NADPH- and O2-dependent hydroxylation reactions. Plants have evolved a large number of different P450 enzymes for the synthesis of secondary metabolites. The F3 'H transcript is most abundant in petals from flowers at an early stage of development and levels decline as the

SEQ ID NO: DNA	SEQ ID NO: polypeptide	Category	Description
			flower matures. Transcripts are also detected in the ovaries, sepals, peduncles, stems and anthers of the petunia plant (Brugliera *et al.*, *Plant J.* 19:441-451, 1999
44	88	Tannin biosynthesis	Homologue of leucoanthocyanidin dioxygenase (LDOX) which is an enzyme in the flavonoid biosynthesis pathway. LDOX is expressed as a late gene in the flavonoid biosynthesis pathway.

All the polynucleotides and polypeptides provided by the present invention are isolated and purified, as those terms are commonly used in the art. Preferably, the polypeptides and polynucleotides are at least about 80% pure, more preferably at least about 90% pure, and most preferably at least about 99% pure.

The word "polynucleotide(s)," as used herein, means a polymeric collection of nucleotides, and includes DNA and corresponding RNA molecules and both single and double stranded molecules, including HnRNA and mRNA molecules, sense and anti-sense strands of DNA and RNA molecules, and comprehends cDNA, genomic DNA, and wholly or partially synthesized polynucleotides. A polynucleotide of the present invention may be an entire gene, or any portion thereof. As used herein, a "gene" is a DNA sequence which codes for a functional protein or RNA molecule. Operable anti-sense polynucleotides may comprise a fragment of the corresponding polynucleotide, and the definition of "polynucleotide" therefore includes all operable anti-sense fragments. Anti-sense polynucleotides and techniques involving anti-sense polynucleotides are well known in the art and are described, for example, in Robinson-Benion *et al.*, *Methods in Enzymol.* 254(23): 363-375, 1995 and Kawasaki *et al.*, *Artific. Organs* 20(8): 836-848, 1996.

In specific embodiments, the present invention provides isolated polynucleotides comprising a sequence of SEQ ID NO: 1-44; polynucleotides comprising variants of SEQ ID NO: 1-44; polynucleotides comprising extended sequences of SEQ ID NO: 1-44 and their variants, oligonucleotide primers and probes corresponding to the sequences set out in SEQ ID NO: 1-44 and their variants, polynucleotides comprising at least a specified number of contiguous residues of any of SEQ ID NO: 1-44 (*x*-mers), and polynucleotides comprising extended sequences which include portions of the sequences set out in SEQ ID NO: 1-44, all

of which are referred to herein, collectively, as "polynucleotides of the present invention." Polynucleotides that comprise complements of such polynucleotide sequences, reverse complements of such polynucleotide sequences, or reverse sequences of such polynucleotide sequences, together with variants of such sequences, are also provided.

The definition of the terms "complement(s)," "reverse complement(s)," and "reverse sequence(s)," as used herein, is best illustrated by the following example. For the sequence 5' AGGACC 3', the complement, reverse complement, and reverse sequence are as follows:

complement	3' TCCTGG 5'
reverse complement	3' GGTCCT 5'
reverse sequence	5' CCAGGA 3'.

Preferably, sequences that are complements of a specifically recited polynucleotide sequence are complementary over the entire length of the specific polynucleotide sequence.

As used herein, the term "*x*-mer," with reference to a specific value of "*x*," refers to a polynucleotide comprising at least a specified number ("*x*") of contiguous residues of: any of the polynucleotides provided in SEQ ID NO: 1-44. The value of *x* may be from about 20 to about 600, depending upon the specific sequence.

Polynucleotides of the present invention comprehend polynucleotides comprising at least a specified number of contiguous residues (*x*-mers) of any of the polynucleotides identified as SEQ ID NO: 1-44, or their variants. Similarly, polypeptides of the present invention comprehend polypeptides comprising at least a specified number of contiguous residues (*x*-mers) of any of the polypeptides identified as SEQ ID NO: 45-88. According to preferred embodiments, the value of *x* is at least 20, more preferably at least 40, more preferably yet at least 60, and most preferably at least 80. Thus, polynucleotides of the present invention include polynucleotides comprising a 20-mer, a 40-mer, a 60-mer, an 80-mer, a 100-mer, a 120-mer, a 150-mer, a 180-mer, a 220-mer, a 250-mer; or a 300-mer, 400-mer, 500-mer or 600-mer of a polynucleotide provided in SEQ ID NO: 1-44, or a variant of one of the polynucleotides corresponding to the polynucleotides provided in SEQ ID NO: 1-44. Polypeptides of the present invention include polypeptides comprising a 20-mer, a 40-mer, a 60-mer, an 80-mer, a 100-mer, a 120-mer, a 150-mer, a 180-mer, a 220-mer, a 250-mer; or a 300-mer, 400-mer, 500-mer or 600-mer of a polypeptide provided in SEQ ID NO: 45-88, or a variant thereof.

The polynucleotides of the present invention were isolated by high throughput sequencing of cDNA libraries prepared from forage grass tissue collected from *Lolium perenne* and *Festuca arundinacea*. Some of the polynucleotides of the present invention may be "partial" sequences, in that they do not represent a full-length gene encoding a full-length polypeptide. Such partial sequences may be extended by analyzing and sequencing various DNA libraries using primers and/or probes and well known hybridization and/or PCR techniques. Partial sequences may be extended until an open reading frame encoding a polypeptide, a full-length polynucleotide and/or gene capable of expressing a polypeptide, or another useful portion of the genome is identified. Such extended sequences, including full-length polynucleotides and genes, are described as "corresponding to" a sequence identified as one of the sequences of SEQ ID NO: 1-44 or a variant thereof, or a portion of one of the sequences of SEQ ID NO: 1-44 or a variant thereof, when the extended polynucleotide comprises an identified sequence or its variant, or an identified contiguous portion (*x*-mer) of one of the sequences of SEQ ID NO: 1-44 or a variant thereof. Similarly, RNA sequences, reverse sequences, complementary sequences, anti-sense sequences and the like, corresponding to the polynucleotides of the present invention, may be routinely ascertained and obtained using the cDNA sequences identified as SEQ ID NO: 1-44.

The polynucleotides identified as SEQ ID NOS: 1-44 contain open reading frames ("ORFs") encoding polypeptides and functional portions of polypeptides. Open reading frames may be identified using techniques that are well known in the art. These techniques include, for example, analysis for the location of known start and stop codons, most likely reading frame identification based on codon frequencies, etc. Suitable tools and software for ORF analysis are well known in the art and include, for example, GeneWise, available from The Sanger Center, Wellcome Trust Genome Campus, Hinxton, Cambridge, CB10 1SA, United Kingdom; Diogenes, available from Computational Biology Centers, University of Minnesota, Academic Health Center, UMHG Box 43 Minneapolis MN 55455; and GRAIL, available from the Informatics Group, Oak Ridge National Laboratories, Oak Ridge, Tennessee TN. Once a partial open reading frame is identified, the polynucleotide may be extended in the area of the partial open reading frame using techniques that are well known in the art until the polynucleotide for the full open reading frame is identified.

The location of ORFs (by nucleotide position) contained within SEQ ID NO: 1-44, and the corresponding amino acid sequences are provided in Table 2 below.

TABLE 2

SEQ ID NO: Polynucleotide	ORF	SEQ ID NO: Polypeptide
1	72-1493	45
2	66-1481	46
3	0-1607	47
4	1-1914	48
5	123-1934	49
6	0-1671	50
7	114-1979	51
8	0-737	52
9	47-1783	53
10	170-2029	54
11	113-1849	55
12	154-1818	56
13	211-1866	57
14	79-1767	58
15	76-1926	59
16	80-1930	60
17	91-1782	61
18	91-1782	62
19	84-1775	63
20	97-2994	64
21	112-3065	65
22	226-1794	66
23	0-1226	67
24	243-1811	68
25	207-1727	69
26	101-1615	70
27	108-1634	71
28	150-1718	72
29	169-1737	73
30	12-1589	74
31	5-1579	75
32	136-1332	76
33	136-1332	77
34	95-836	78
35	95-1123	79

SEQ ID NO: Polynucleotide	ORF	SEQ ID NO: Polypeptide
36	82-847	80
37	82-1104	81
38	0-1532	82
39	58-1632	83
40	0-1580	84
41	16-1596	85
42	0-1478	86
43	20-1519	87
44	117-1259	88

Once open reading frames are identified, the open reading frames may be isolated and/or synthesized. Expressible genetic constructs comprising the open reading frames and suitable promoters, initiators, terminators, etc., which are well known in the art, may then be constructed. Such genetic constructs may be introduced into a host cell to express the polypeptide encoded by the open reading frame. Suitable host cells may include various prokaryotic and eukaryotic cells, including plant cells, mammalian cells, bacterial cells, algae and the like.

The polynucleotides of the present invention may be isolated by high throughput sequencing of cDNA libraries prepared from forage grass tissue, as described below in Example 1. Alternatively, oligonucleotide probes and primers based on the sequences provided in SEQ ID NO: 1-44 can be synthesized as detailed below, and used to identify positive clones in either cDNA or genomic DNA libraries from forage grass tissue cells by means of hybridization or polymerase chain reaction (PCR) techniques. Hybridization and PCR techniques suitable for use with such oligonucleotide probes are well known in the art (*see*, for example, Mullis *et al.*, *Cold Spring Harbor Symp. Quant. Biol.*, 51:263, 1987; Erlich, ed., *PCR technology*, Stockton Press: NY, 1989; and Sambrook *et al.*, eds., *Molecular cloning: a laboratory manual*, 2nd ed., CSHL Press: Cold Spring Harbor, NY, 1989). In addition to DNA-DNA hybridization, DNA-RNA or RNA-RNA hybridization assays are also possible. In the first case, the mRNA from expressed genes would then be detected instead of genomic DNA or cDNA derived from mRNA of the sample. In the second case, RNA probes could be used. Artificial analogs of DNA hybridizing specifically to target

sequences could also be employed. Positive clones may be analyzed by restriction enzyme digestion, DNA sequencing or the like.

The polynucleotides of the present invention may also, or alternatively, be synthesized using techniques that are well known in the art. The polynucleotides may be synthesized, for example, using automated oligonucleotide synthesizers (*e.g.*, Beckman Oligo 1000M DNA Synthesizer; Beckman Coulter Ltd., Fullerton, CA) to obtain polynucleotide segments of up to 50 or more nucleic acids. A plurality of such polynucleotide segments may then be ligated using standard DNA manipulation techniques that are well known in the art of molecular biology. One conventional and exemplary polynucleotide synthesis technique involves synthesis of a single stranded polynucleotide segment having, for example, 80 nucleic acids, and hybridizing that segment to a synthesized complementary 85 nucleic acid segment to produce a 5 nucleotide overhang. The next segment may then be synthesized in a similar fashion, with a 5 nucleotide overhang on the opposite strand. The "sticky" ends ensure proper ligation when the two portions are hybridized. In this way, a complete polynucleotide of the present invention may be synthesized entirely *in vitro*.

Oligonucleotide probes and primers complementary to and/or corresponding to SEQ ID NO: 1-44 and variants of those sequences, are also comprehended by the present invention. Such oligonucleotide probes and primers are substantially complementary to the polynucleotide of interest over a certain portion of the polynucleotide. An oligonucleotide probe or primer is described as "corresponding to" a polynucleotide of the present invention, including one of the sequences set out as SEQ ID NO: 1-44 or a variant thereof, if the oligonucleotide probe or primer, or its complement, is contained within one of the sequences set out as SEQ ID NOS: 1-44 or a variant of one of the specified sequences.

Two single stranded sequences are said to be substantially complementary when the nucleotides of one strand, optimally aligned and compared, with the appropriate nucleotide insertions and/or deletions, pair with at least 80%, preferably at least 90% to 95%, and more preferably at least 98% to 100%, of the nucleotides of the other strand. Alternatively, substantial complementarity exists when a first DNA strand will selectively hybridize to a second DNA strand under stringent hybridization conditions.

In specific embodiments, the inventive oligonucleotide probes and/or primers comprise at least about 6 contiguous residues, more preferably at least about 10 contiguous

residues, and most preferably at least about 20 contiguous residues complementary to a polynucleotide sequence of the present invention. Probes and primers of the present invention may be from about 8 to 100 base pairs in length, preferably from about 10 to 50 base pairs in length, and more preferably from about 15 to 40 base pairs in length. The probes can be easily selected using procedures well known in the art, taking into account DNA-DNA hybridization stringencies, annealing and melting temperatures, potential for formation of loops, and other factors which are well known in the art. Preferred techniques for designing PCR primers are disclosed in Dieffenbach and Dyksler, *PCR Primer: a laboratory manual*, CSHL Press: Cold Spring Harbor, NY, 1995. A software program suitable for designing probes, and especially for designing PCR primers, is available from Premier Biosoft International, 3786 Corina Way, Palo Alto, CA 94303-4504.

The isolated polynucleotides of the present invention also have utility in genome mapping, in physical mapping, and in positional cloning of genes.

The polynucleotides identified as SEQ ID NO: 1-44 were isolated from cDNA clones and represent sequences that are expressed in the tissue from which the cDNA was prepared. RNA sequences, reverse sequences, complementary sequences, anti-sense sequences, and the like, corresponding to the polynucleotides of the present invention, may be routinely ascertained and obtained using the cDNA sequences identified as SEQ ID NO: 1-44.

Identification of genomic DNA and heterologous species DNA can be accomplished by standard DNA/DNA hybridization techniques, under appropriately stringent conditions, using all or part of a polynucleotide sequence as a probe to screen an appropriate library. Alternatively, PCR techniques using oligonucleotide primers that are designed based on known genomic DNA, cDNA and protein sequences can be used to amplify and identify genomic and cDNA sequences.

In another aspect, the present invention provides isolated polypeptides encoded by the above polynucleotides. As used herein, the term “polypeptide” encompasses amino acid chains of any length, including full-length proteins, wherein the amino acid residues are linked by covalent peptide bonds. The term “polypeptide encoded by a polynucleotide” as used herein, includes polypeptides encoded by a polynucleotide that comprises a partial isolated polynucleotide sequence provided herein. In specific embodiments, the inventive

polypeptides comprise an amino acid sequence selected from the group consisting of SEQ ID NO: 45-88, as well as variants of such sequences.

As noted above, polypeptides of the present invention may be produced recombinantly by inserting a polynucleotide sequence encoding the polypeptide into an expression vector and expressing the polypeptide in an appropriate host. Any of a variety of expression vectors known to those of ordinary skill in the art may be employed. Expression may be achieved in any appropriate host cell that has been transformed or transfected with an expression vector containing a polynucleotide molecule that encodes a recombinant polypeptide. Suitable host cells include prokaryotes, yeast, and higher eukaryotic cells. Preferably, the host cells employed are plant, *E. coli*, insect, yeast, or a mammalian cell line such as COS or CHO. The polynucleotide sequences expressed in this manner may encode naturally occurring polypeptides, portions of naturally occurring polypeptides, or other variants thereof. The expressed polypeptides may be used in various assays known in the art to determine their biological activity. Such polypeptides may also be used to raise antibodies, to isolate corresponding interacting proteins or other compounds, and to quantitatively determine levels of interacting proteins or other compounds.

In a related aspect, polypeptides are provided that comprise at least a functional portion of a polypeptide having an amino acid sequence selected from the group consisting of sequences provided in SEQ ID NO: 45-88 and variants thereof. As used herein, the "functional portion" of a polypeptide is that portion which contains an active site essential for affecting the function of the polypeptide, for example, a portion of the molecule that is capable of binding one or more reactants. The active site may be made up of separate portions present on one or more polypeptide chains and will generally exhibit high binding affinity. Functional portions of a polypeptide may be identified by first preparing fragments of the polypeptide by either chemical or enzymatic digestion of the polypeptide, or by mutation analysis of the polynucleotide that encodes the polypeptide and subsequent expression of the resulting mutant polypeptides. The polypeptide fragments or mutant polypeptides are then tested to determine which portions retain biological activity, using methods well known to those of skill in the art, including the representative assays described below.

Portions and other variants of the inventive polypeptides may be generated by synthetic or recombinant means. Synthetic polypeptides having fewer than about 100 amino acids, and generally fewer than about 50 amino acids, may be generated using techniques well known to those of ordinary skill in the art. For example, such polypeptides may be synthesized using any of the commercially available solid-phase techniques, such as the Merrifield solid-phase synthesis method, where amino acids are sequentially added to a growing amino acid chain. *See* Merrifield, *J. Am. Chem. Soc.* 85: 2149-2146, 1963. Equipment for automated synthesis of polypeptides is commercially available from suppliers such as Perkin Elmer/Applied Biosystems, Inc. (Foster City, California), and may be operated according to the manufacturer's instructions. Variants of a native polypeptide may be prepared using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis (Kunkel, *Proc. Natl. Acad. Sci. USA* 82: 488-492, 1985). Sections of DNA sequences may also be removed using standard techniques to permit preparation of truncated polypeptides.

As used herein, the term "variant" comprehends nucleotide or amino acid sequences different from the specifically identified sequences, wherein one or more nucleotides or amino acid residues is deleted, substituted, or added. Variants may be naturally occurring allelic variants, or non-naturally occurring variants. Variant sequences (polynucleotide or polypeptide) preferably exhibit at least 75%, more preferably at least 80%, more preferably at least 90%, more preferably yet at least 95%, and most preferably at least 98% identity to a sequence of the present invention. The percentage identity is determined by aligning the two sequences to be compared as described below, determining the number of identical residues in the aligned portion, dividing that number by the total number of residues in the inventive (queried) sequence, and multiplying the result by 100.

Polynucleotides and polypeptides having a specified percentage identity to a polynucleotide or polypeptide identified in one of SEQ ID NO: 1-88 thus share a high degree of similarity in their primary structure. In addition to a specified percentage identity to a polynucleotide of the present invention, variant polynucleotides and polypeptides preferably have additional structural and/or functional features in common with a polynucleotide of the present invention. Polynucleotides having a specified degree of identity to, or capable of hybridizing to, a polynucleotide of the present invention preferably additionally have at least

one of the following features: (1) they contain an open reading frame, or partial open reading frame, encoding a polypeptide, or a functional portion of a polypeptide, having substantially the same functional properties as the polypeptide, or functional portion thereof, encoded by a polynucleotide in a recited SEQ ID NO:; or (2) they contain identifiable domains in common.

Polynucleotide or polypeptide sequences may be aligned, and percentages of identical nucleotides or amino acids in a specified region may be determined against another polynucleotide or polypeptide, using computer algorithms that are publicly available. For example, the BLASTN and FASTA algorithms, set to the default parameters described in the documentation and distributed with the algorithm, may be used for aligning and identifying the similarity of polynucleotide sequences. The alignment and similarity of polypeptide sequences may be examined using the BLASTP algorithm. BLASTX and FASTX algorithms compare nucleotide query sequences translated in all reading frames against polypeptide sequences. The FASTA and FASTX algorithms are described in Pearson and Lipman, *Proc. Natl. Acad. Sci. USA* 85:2444-2448, 1988; and in Pearson, *Methods in Enzymol.* 183:63-98, 1990. The FASTA software package is available from the University of Virginia by contacting the Assistant Provost for Research, University of Virginia, PO Box 9025, Charlottesville, VA 22906-9025. The BLASTN software is available from the National Center for Biotechnology Information (NCBI), National Library of Medicine, Building 38A, Room 8N805, Bethesda, MD 20894. The BLASTN algorithm Version 2.0.11 [Jan-20-2000] set to the default parameters described in the documentation and distributed with the algorithm, is preferred for use in the determination of polynucleotide variants according to the present invention. The use of the BLAST family of algorithms, including BLASTN, BLASTP and BLASTX, is described in the publication of Altschul *et al.*, "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs," *Nucleic Acids Res*. 25:3389-3402, 1997.

The following running parameters are preferred for determination of alignments and similarities using BLASTN that contribute to the percentage identity and E values for polynucleotides: Unix running command with the following default parameters: blastall -p blastn -d embldb -e 10 -G 0 -E 0 -r 1 -v 30 -b 30 -i queryseq –o results; and parameters are: -p Program Name [String]; -d Database [String]; -e Expectation value (E) [Real]; -G Cost to open a gap (zero invokes default behavior) [Integer]; -FF low complexity filter; -E Cost to

extend a gap (zero invokes default behavior) [Integer]; -r Reward for a nucleotide match (BLASTN only) [Integer]; -v Number of one-line descriptions (V) [Integer]; -b Number of alignments to show (B) [Integer]; -i Query File [File In]; -o BLAST report Output File [File Out] Optional.

The following running parameters are preferred for determination of alignments and similarities using BLASTP that contribute to the percentage identity and E values of polypeptide sequences: blastall –p blastp –d swissprotdb –e 10 -G 0 -E 0 -FF –v 30 –b 30 –i queryseq –o results; the parameters are: -p Program Name [String]; -d Database [String]; -e Expectation value (E) [Real]; -G Cost to open a gap (zero invokes default behavior) [Integer]; -FF low complexity filter; -E Cost to extend a gap (zero invokes default behavior) [Integer]; -v Number of one-line descriptions (v) [Integer]; -b Number of alignments to show (b) [Integer]; -I Query File [File In]; -o BLAST report Output File [File Out] Optional.

The "hits" to one or more database sequences by a queried sequence produced by BLASTN, BLASTP, FASTA or a similar algorithm, align and identify similar portions of sequences. The hits are arranged in order of the degree of similarity and the length of sequence overlap. Hits to a database sequence generally represent an overlap over only a fraction of the sequence length of the queried sequence.

As noted above, the percentage identity of a polynucleotide or polypeptide sequence is determined by aligning polynucleotide and polypeptide sequences using appropriate algorithms, such as BLASTN or BLASTP, respectively, set to default parameters; identifying the number of identical nucleic or amino acids over the aligned portions; dividing the number of identical nucleic or amino acids by the total number of nucleic or amino acids of the polynucleotide or polypeptide of the present invention; and then multiplying by 100 to determine the percentage identity. By way of example, a queried polynucleotide having 220 nucleic acids has a hit to a polynucleotide sequence in the EMBL database having 520 nucleic acids over a stretch of 23 nucleotides in the alignment produced by the BLASTN algorithm using the default parameters. The 23-nucleotide hit includes 21 identical nucleotides, one gap and one different nucleotide. The percentage identity of the queried polynucleotide to the hit in the EMBL database is thus 21/220 times 100, or 9.5%. The percentage identity of polypeptide sequences may be determined in a similar fashion.

The BLASTN and BLASTX algorithms also produce "Expect" values for polynucleotide and polypeptide alignments. The Expect value (E) indicates the number of hits one can "expect" to see over a certain number of contiguous sequences by chance when searching a database of a certain size. The Expect value is used as a significance threshold for determining whether the hit to a database indicates true similarity. For example, an E value of 0.1 assigned to a polynucleotide hit is interpreted as meaning that in a database of the size of the EMBL database, one might expect to see 0.1 matches over the aligned portion of the sequence with a similar score simply by chance. By this criterion, the aligned and matched portions of the sequences then have a probability of 90% of being related. For sequences having an E value of 0.01 or less over aligned and matched portions, the probability of finding a match by chance in the EMBL database is 1% or less using the BLASTN algorithm. E values for polypeptide sequences may be determined in a similar fashion using various polypeptide databases, such as the SwissProt database.

According to one embodiment, "variant" polynucleotides and polypeptides, with reference to each of the polynucleotides and polypeptides of the present invention, preferably comprise sequences having the same number or fewer nucleotides or amino acids than each of the polynucleotides or polypeptides of the present invention and producing an E value of 0.01 or less when compared to the polynucleotide or polypeptide of the present invention. That is, a variant polynucleotide or polypeptide is any sequence that has at least a 99% probability of being related to the polynucleotide or polypeptide of the present invention, measured as having an E value of 0.01 or less using the BLASTN or BLASTX algorithms set at the default parameters. According to a preferred embodiment, a variant polynucleotide is a sequence having the same number or fewer nucleic acids than a polynucleotide of the present invention that has at least a 99% probability of being related to the polynucleotide of the present invention, measured as having an E value of 0.01 or less using the BLASTN algorithm set at the default parameters. Similarly, according to a preferred embodiment, a variant polypeptide is a sequence having the same number or fewer amino acids than a polypeptide of the present invention that has at least a 99% probability of being related as the polypeptide of the present invention, measured as having an E value of 0.01 or less using the BLASTP algorithm set at the default parameters.

In an alternative embodiment, variant polynucleotides are sequences that hybridize to a polynucleotide of the present invention under stringent conditions. Stringent hybridization conditions for determining complementarity include salt conditions of less than about 1 M, more usually less than about 500 mM, and preferably less than about 200 mM. Hybridization temperatures can be as low as 5°C, but are generally greater than about 22°C, more preferably greater than about 30°C, and most preferably greater than about 37°C. Longer DNA fragments may require higher hybridization temperatures for specific hybridization. Since the stringency of hybridization may be affected by other factors such as probe composition, presence of organic solvents, and extent of base mismatching, the combination of parameters is more important than the absolute measure of any one alone. An example of "stringent conditions" is prewashing in a solution of 6X SSC, 0.2% SDS; hybridizing at 65°C, 6X SSC, 0.2% SDS overnight; followed by two washes of 30 minutes each in 1X SSC, 0.1% SDS at 65°C and two washes of 30 minutes each in 0.2X SSC, 0.1% SDS at 65°C.

The present invention also encompasses polynucleotides that differ from the disclosed sequences but that, as a consequence of the discrepancy of the genetic code, encode a polypeptide having similar enzymatic activity to a polypeptide encoded by a polynucleotide of the present invention. Thus, polynucleotides comprising sequences that differ from the polynucleotide sequences recited in SEQ ID NO: 1-44, or complements, reverse sequences, or reverse complements of those sequences, as a result of conservative substitutions are contemplated by and encompassed within the present invention. Additionally, polynucleotides comprising sequences that differ from the polynucleotide sequences recited in SEQ ID NO: 1-44, or complements, reverse complements or reverse sequences thereof, as a result of deletions and/or insertions totaling less than 10% of the total sequence length are also contemplated by and encompassed within the present invention. Similarly, polypeptides comprising sequences that differ from the polypeptide sequences recited in SEQ ID NO: 45-88 as a result of amino acid substitutions, insertions, and/or deletions totaling less than 10% of the total sequence length are contemplated by and encompassed within the present invention, provided the variant polypeptide has activity in a fructan, cellulose, starch and/or tannin biosynthetic pathway.

In another aspect, the present invention provides genetic constructs comprising, in the 5'-3' direction, a gene promoter sequence; an open reading frame coding for at least a functional portion of a polypeptide of the present invention; and a gene termination sequence. The open reading frame may be orientated in either a sense or anti-sense direction. For applications where amplification of fructan, cellulose, starch or tannin synthesis is desired, the open reading frame may be inserted in the construct in a sense orientation, such that transformation of a target organism with the construct will lead to an increase in the number of copies of the gene and therefore an increase in the amount of enzyme. When down-regulation of fructan, cellulose, starch or tannin synthesis is desired, the open reading frame may be inserted in the construct in an anti-sense orientation, such that the RNA produced by transcription of the polynucleotide is complementary to the endogenous mRNA sequence. This, in turn, will result in a decrease in the number of copies of the gene and therefore a decrease in the amount of enzyme. Alternatively, regulation may be achieved by inserting appropriate sequences or subsequences (*e.g.*, DNA or RNA) in ribozyme constructs.

Genetic constructs comprising a non-coding region of a gene coding for a polypeptide of the present invention, or a nucleotide sequence complementary to a non-coding region, together with a gene promoter sequence and a gene termination sequence, are also provided. As used herein the term "non-coding region" includes both transcribed sequences which are not translated, and non-transcribed sequences within about 2000 base pairs 5' or 3' of the translated sequences or open reading frames. Examples of non-coding regions which may be usefully employed in the inventive constructs include introns and 5'- non-coding leader sequences. Transformation of a target plant with such a genetic construct may lead to a reduction in the amount of fructan, cellulose, starch or tannin synthesized by the plant by the process of cosuppression, in a manner similar to that discussed, for example, by Napoli *et al.*, *Plant Cell* 2:279-290, 1990; and de Carvalho Niebel *et al.*, *Plant Cell* 7:347-358, 1995.

The genetic constructs of the present invention further comprise a gene promoter sequence and a gene termination sequence, operably linked to the polynucleotide to be transcribed, which control expression of the gene. The gene promoter sequence is generally positioned at the 5' end of the polynucleotide to be transcribed, and is employed to initiate transcription of the polynucleotide. Gene promoter sequences are generally found in the 5' non-coding region of a gene but they may exist in introns (Luehrsen, *Mol. Gen. Genet.*

225:81-93, 1991) or in the coding region, as for example in PAL of tomato (Bloksberg, *Studies on the Biology of Phenylalanine Ammonia Lyase and Plant Pathogen Interaction*, Ph.D. Thesis, University of California, Davis, 1991, University Microfilms International Order No. 9217564). When the construct includes an open reading frame in a sense orientation, the gene promoter sequence also initiates translation of the open reading frame. For genetic constructs comprising either an open reading frame in an anti-sense orientation or a non-coding region, the gene promoter sequence consists only of a transcription initiation site having a RNA polymerase binding site.

A variety of gene promoter sequences which may be usefully employed in the genetic constructs of the present invention are well known in the art. The promoter gene sequence, and also the gene termination sequence, may be endogenous to the target plant host or may be exogenous, provided the promoter is functional in the target host. For example, the promoter and termination sequences may be from other plant species, plant viruses, bacterial plasmids and the like. Preferably, gene promoter and termination sequences are from the inventive sequences themselves.

Factors influencing the choice of promoter include the desired tissue specificity of the construct, and the timing of transcription and translation. For example, constitutive promoters, such as the 35S Cauliflower Mosaic Virus (CaMV 35S) promoter or the superubiquitin promoter (PCT International Patent Publication WO 00/58474), will affect the activity of the enzyme in all parts of the plant. Use of a tissue specific promoter will result in production of the desired sense or anti-sense RNA only in the tissue of interest. With DNA constructs employing inducible gene promoter sequences, the rate of RNA polymerase binding and initiation can be modulated by external stimuli, such as light, heat, anaerobic stress, alteration in nutrient conditions and the like. Temporally regulated promoters can be employed to effect modulation of the rate of RNA polymerase binding and initiation at a specific time during development of a transformed cell. Preferably, the original promoters from the enzyme gene in question, or promoters from a specific tissue-targeted gene in the organism to be transformed, such as *Lolium* or *Festuca*, are used. Grass promoters different from the original gene may also be usefully employed in the inventive genetic constructs in order to prevent feedback inhibition. For example, the fructosyltransferase gene will be regulated by sucrose sensing systems; therefore removing the gene from under control of its

normal promoter allows the gene to be active all the time. Other examples of gene promoters which may be usefully employed in the present invention include, mannopine synthase (mas), octopine synthase (ocs) and those reviewed by Chua *et al., Science* 244:174-181, 1989.

The gene termination sequence, which is located 3' to the polynucleotide to be transcribed, may come from the same gene as the gene promoter sequence or may be from a different gene. Many gene termination sequences known in the art may be usefully employed in the present invention, such as the 3' end of the *Agrobacterium tumefaciens* nopaline synthase gene. However, preferred gene terminator sequences are those from the original enzyme gene or from the target species to be transformed.

The genetic constructs of the present invention may also contain a selection marker that is effective in plant cells, to allow for the detection of transformed cells containing the inventive construct. Such markers, which are well known in the art, typically confer resistance to one or more toxins. One example of such a marker is the NPTII gene whose expression results in resistance to kanamycin or hygromycin, antibiotics which are usually toxic to plant cells at a moderate concentration (Rogers *et al., in* Weissbach A and H, eds., *Methods for Plant Molecular Biology*, Academic Press Inc.: San Diego, CA, 1988). Alternatively, the presence of the desired construct in transformed cells can be determined by means of other techniques well known in the art, such as Southern and Western blots.

Techniques for operatively linking the components of the inventive genetic constructs are well known in the art and include the use of synthetic linkers containing one or more restriction endonuclease sites as described, for example, by Sambrook *et al.*, (*Molecular cloning: a laboratory manual*, CSHL Press: Cold Spring Harbor, NY, 1989). The genetic construct of the present invention may be linked to a vector having at least one replication system, for example, *E. coli*, whereby after each manipulation, the resulting construct can be cloned and sequenced, and the correctness of the manipulation determined.

The genetic constructs of the present invention may be used to transform a variety of plants, both monocotyledonous (*e.g.*, grasses, maize/corn, grains, oats, rice, sorghum, millet, rye, sugar cane, wheat and barley), dicotyledonous (*e.g.*, *Arabidopsis*, tobacco, legumes, alfalfa, oaks, eucalyptus, maple), and gymnosperms. In a preferred embodiment, the inventive genetic constructs are employed to transform grasses. Preferably the target plant is

selected from the group consisting of *Lolium* and *Festuca* species, most preferably from the group consisting of *Lolium perenne and Festuca arundinacea*. Plants that may be usefully transformed with the inventive genetic constructs include other species of ryegrass and fescue, including, but not limited to *Lolium multiflorum* (Italian ryegrass), *Lolium hybridum* (hybrid ryegrass), *Lolium rigidum* (Wimerra grass), *Lolium temulentum* (darnel), *Festuca rubra* (red fescue) and *Festuca pratensis* (meadow fescue). As discussed above, transformation of a plant with a genetic construct of the present invention will produce a modified fructan, cellulose, starch or tannin content in the plant.

The production of RNA in target cells may be controlled by choice of the promoter sequence, or by selecting the number of functional copies or the site of integration of the polynucleotides incorporated into the genome of the target organism. A target plant may be transformed with more than one construct of the present invention, thereby modulating the fructan, cellulose, starch and/or tannin biosynthetic pathways by affecting the activity of more than one enzyme, affecting enzyme activity in more than one tissue, or affecting enzyme activity at more than one expression time. Similarly, a construct may be assembled containing more than one open reading frame coding for an enzyme encoded by a polynucleotide of the present invention or more than one non-coding region of a gene coding for such an enzyme. The polynucleotides of the present invention may also be employed in combination with other known sequences encoding enzymes involved in the lignin, fructan and/or tannin biosynthetic pathways. In this manner, more than one biosynthetic pathway may be modulated, or a fructan, cellulose, starch or tannin biosynthetic pathway may be added to a plant to produce a plant having an altered phenotype.

Techniques for stably incorporating genetic constructs into the genome of target plants are well known in the art and include *Agrobacterium tumefaciens* mediated introduction, electroporation, protoplast fusion, injection into reproductive organs, injection into immature embryos, high velocity projectile introduction and the like. The choice of technique will depend upon the target plant to be transformed. For example, dicotyledonous plants, and certain monocots and gymnosperms may be transformed by *Agrobacterium* Ti plasmid technology, as described, for example by Bevan, *Nucleic Acid Res*. 12:8711-8721, 1984. Targets for the introduction of the genetic constructs of the present invention include tissues, such as leaf tissue, disseminated cells, protoplasts, seeds, embryos, meristematic

regions; cotyledons, hypocotyls, and the like. Transformation techniques which may be usefully employed in the inventive methods include those taught by Ellis *et al., Plant Cell Reports*, 8:16-20, 1989; Wilson *et al., Plant Cell Reports* 7:704-707, 1989; and Tautorus *et al., Theor. Appl. Genet.* 78:531-536, 1989.

Once the cells are transformed, cells having the inventive genetic construct incorporated in their genome may be selected by means of a marker, such as the kanamycin resistance marker discussed above. Transgenic cells may then be cultured in an appropriate medium to regenerate whole plants, using techniques well known in the art. In the case of protoplasts, the cell wall is allowed to reform under appropriate osmotic conditions. In the case of seeds or embryos, an appropriate germination or callus initiation medium is employed. For explants, an appropriate regeneration medium is used. Regeneration of plants is well established for many species. The resulting transformed plants may be reproduced sexually or asexually, using methods well known in the art, to give successive generations of transgenic plants.

Polynucleotides of the present invention may also be used to specifically suppress gene expression by methods that operate post-transcriptionally to block the synthesis of products of targeted genes, such as RNA interference (RNAi), and quelling. Briefly, traditional methods of gene suppression, employing anti-sense RNA or DNA, operate by binding to the reverse sequence of a gene of interest such that binding interferes with subsequent cellular processes and therefore blocks synthesis of the corresponding protein. RNAi also operates on a post-translational level and is sequence specific, but suppresses gene expression far more efficiently. Exemplary methods for controlling or modifying gene expression using RNAi are provided in US Patent 6,506,559 and PCT International Publications WO 99/49029 and WO 99/53050. In these methods, post-transcriptional gene silencing is brought about by a sequence-specific RNA degradation process which results in the rapid degradation of transcripts of sequence-related genes. Studies have shown that double-stranded RNA may act as a mediator of sequence-specific gene silencing (see, for example, Montgomery and Fire, *Trends in Genetics*, 14:255-258, 1998). Gene constructs that produce transcripts with self-complementary regions are particularly efficient at gene silencing. A unique feature of this post-transcriptional gene silencing pathway is that silencing is not limited to the cells where it is initiated. The gene-silencing effects may be

disseminated to other parts of an organism and even transmitted through the germ line to several generations.

The polynucleotides of the present invention may thus be employed to generate gene silencing constructs and/or gene-specific self-complementary RNA sequences that can be delivered by conventional art-known methods to plant tissues, such as forage grass tissues. Within genetic constructs, sense and antisense sequences can be placed in regions flanking an intron sequence in proper splicing orientation with donor and acceptor splicing sites, such that intron sequences are removed during processing of the transcript, and sense and antisense sequences, as well as splice junction sequences, bind together to form double-stranded RNA. Alternatively, spacer sequences of various lengths may be employed to separate self-complementary regions of sequence in the construct. During processing of the gene construct transcript, intron sequences are spliced-out, allowing sense and anti-sense sequences, as well as splice junction sequences, to bind forming double-stranded RNA. Select ribonucleases then bind to and cleave the double-stranded RNA, thereby initiating the cascade of events leading to degradation of specific mRNA gene sequences, and silencing specific genes. Alternatively, rather than using a gene construct to express the self-complementary RNA sequences, the gene-specific double-stranded RNA segments are delivered to one or more targeted areas to be internalized into the cell cytoplasm to exert a gene silencing effect. The double-stranded RNA must have sufficient homology to the targeted gene to mediate RNAi and is preferably at least 25 nucleotides in length. Preferably, the double-stranded RNA corresponds specifically to a polynucleotide of the present invention. Gene silencing RNA sequences comprising the polynucleotides of the present invention are useful for creating genetically modified plants with desired phenotypes as well as for characterizing genes (for example, in high-throughput screening of sequences), and studying their functions in intact organisms.

Example 1

ISOLATION OF cDNA SEQUENCES FROM *L. PERENNE* AND *F. ARUNDINACEA* cDNA LIBRARIES

L. perenne and *F. arundinacea* cDNA expression libraries were constructed and screened as follows. Tissue was collected from *L. perenne* and *F. arundinacea* during winter and spring, and snap-frozen in liquid nitrogen. The tissues collected included those obtained from leaves, pseudostem, roots, inflorescence (day 0), stem bases from day 7 emerged inflorescence, basal leaf day 3 and day 6, floral stem and vegetative stem. Total RNA was isolated from each tissue type using TRIzol Reagent (BRL Life Technologies, Gaithersburg, MD). mRNA from each tissue type was obtained using a Poly(A) Quik mRNA isolation kit (Stratagene, La Jolla, CA), according to the manufacturer's specifications. cDNA expression libraries were constructed from the purified mRNA by reverse transcriptase synthesis followed by insertion of the resulting cDNA in Lambda ZAP using a ZAP Express cDNA Synthesis Kit (Stratagene), according to the manufacturer's protocol. The resulting cDNA clones were packaged using a Gigapack II Packaging Extract (Stratagene) employing 1 μl of sample DNA from the 5 μl ligation mix. Mass excision of the libraries was performed using XL1-Blue MRF' cells and XLOLR cells (Stratagene) with ExAssist helper phage (Stratagene). The excised phagemids were diluted with NZY broth (Gibco BRL, Gaithersburg, MD) and plated out onto LB-kanamycin agar plates containing 5-bromo-4-chloro-3-indolyl-beta-D-galactosidase (X-gal) and isopropylthio-beta-galactoside (IPTG).

Of the colonies plated and picked for DNA preparations, the large majority contained an insert suitable for sequencing. Positive colonies were cultured in NZY broth with kanamycin and DNA was purified following standard protocols. Agarose gel at 1% was used to screen sequencing templates for chromosomal contamination. Dye terminator sequences were prepared using a Biomek 2000 robot (Beckman Coulter Inc., Fullerton, CA) for liquid handling and DNA amplification using a 9700 PCR machine (Perkin Elmer/Applied Biosystems, Foster City, CA) according to the manufacturer's protocol.

The DNA sequences for positive clones were obtained using a Perkin Elmer/Applied Biosystems Division Prism 377 sequencer. cDNA clones were sequenced from the 5' end. The polynucleotide sequences identified as SEQ ID NO: 1, 3-5, 8-15, 17, 18, 20, 25, 27, 28,

30, 36-39 and 44 were identified from *Lolium perenne* cDNA expression libraries, with the polynucleotides of SEQ ID NO: 2, 6, 7, 16, 19, 21-24, 26, 29, 31-35 and 40-43 being identified from *Festuca arundinacea* cDNA expression libraries.

BLASTN Polynucleotide Analysis

The isolated cDNA sequences were compared to sequences in the EMBL DNA database using the computer algorithm BLASTN. Comparisons of DNA sequences provided in SEQ ID NO: 1-44 to sequences in the EMBL DNA database were made as of April 28, 2003, using BLASTN algorithm Version 2.0.11 [Jan-20-2000], and the following Unix running command: blastall –p blastn –d embldb –e 10 -FF –G0 –E0 –r 1 –v 30 –b 30 –i queryseq –o.

The sequences of SEQ ID NO: 6-9, 11-19, 21, 25-27 and 34-44 were determined to have less than 50% identity, determined as described above using the computer algorithm BLASTN, to sequences in the EMBL database. The sequence of SEQ ID NO: 3, 4, 10, 20, 22-24, 28, 29 and 31-33 was determined to have less than 75% identity, determined as described above, to sequences in the EMBL database, using the computer algorithm BLASTN, as described above. The sequences of SEQ ID NO: 1, 2 and 30 were determined to have less than 90% identity to sequences in the EMBL database using the computer algorithm BLASTN, as described above. Finally, the sequence of SEQ ID NO: 5 were determined to have less than 98% identity to sequences in the EMBL database using the computer algorithm BLASTN, as described above.

BLASTP Polypeptide Analysis

The isolated sequences were compared to sequences in the SwissProt protein database using the computer algorithm BLASTP. Specifically, comparisons of polypeptide sequences provided in SEQ ID NO: 45-88 to sequences in the SwissProt protein database were made as of April 28, 2003, using BLASTP algorithm Version 2.0.11 [Jan-20-2000], and the following Unix running command: blastall –p blastp –d swissprotdb –e 10 -FF –G0 –E0 –v 30 –b 30 –i queryseq –o.

The sequences of SEQ ID NO: 78-81 were determined to have less than 50% identity to sequences in the SwissProt database using the computer algorithm BLASTP as described

above. The sequences of SEQ ID NO: 51, 53, 55, 56, 71, 83 and 88 were determined to have less than 75% identity to sequences in the SwissProt database using the computer algorithm BLASTP, as described above. The sequences of SEQ ID NO: 50, 52, 54, 57-68, 82 and 84-87 were determined to have less than 90% identity to sequences in the SwissProt database using the computer algorithm BLASTP, as described above. Finally, the sequences of SEQ ID NO: 45-49, 69, 70 and 72-77 were determined to have less than 98% identity to sequences in the SwissProt database using the computer algorithm BLASTP, as described above.

BLASTX Polynucleotide Analysis

The isolated cDNA sequences were compared to sequences in the SwissProt protein database using the computer algorithm BLASTX. Comparisons of DNA sequences provided in SEQ ID NOS: 1-44, to sequences in the SwissProt DNA database (using BLASTX) were made as of April 28, 2003, using BLAST algorithm Version 2.0.11 [Jan-20-2000], and the following Unix running command: blastall –p blastx –d swissprotdb –e 10 –FF –G0 –E0 –r 1 –v 30 –b 30 –i queryseq –o.

The sequences of SEQ ID NO: 27 and 34-37 were determined to have less than 50% identity, determined as described above, to sequences in the SwissProt database using the computer algorithm BLASTX, as described above. The sequences of SEQ ID NO: 3, 4, 6-19, 21-26, 28, 29, 33 and 38-44 were determined to have less than 75% identity, determined as described above, to sequences in the SwissProt database using the computer algorithm BLASTX, as described above. Finally, the sequences of SEQ ID NO: 1, 2, 5, 20 and 30-32 were determined to have less than 90% identity, determined as described above, to sequences in the SwissProt database using the computer algorithm BLASTX, as described above.

Figs. 3-41 show the positions of domains within the amino acid sequences of SEQ ID NO: 45-48, 53-70 and 72-88, respectively. These domains were determined with InterProScan software Release v3.1, November 6, 2001. The InterPro database integrates PROSITE, PRINTS, Pfam, ProDom, SMART and TIGRFAMs databases, and the addition of others is scheduled. InterPro data is distributed in XML format and it is freely available under the InterPro Consortium copyright. The European Bioinformatics Institute (EBI) is a

non-profit academic organization that forms part of the European Molecular Biology Laboratory (EMBL): Wellcome Trust Genome Campus, Hinxton, Cambridge, CB10 1SD UK.

Example 2

USE OF CHALCONE SYNTHASE GENES TO MODIFY TANNIN BIOSYNTHESIS

Certain *Arabidopsis* mutants of the *transparent testa* (*tt*) phenotype do not make the anthocyanin pigment cyanidin and therefore have no seed coat color. The genes responsible for many of these mutants have now been identified as shown in Table 3.

TABLE 3

Enzyme	Abbreviation	Locus	Chromosome
Dihydroflavanol-4-reductase	DFR	*tt3*	5
Chalcone synthase	CHS	*tt4*	5
Chalcone isomerase	CHI	*tt5*	3
Flavanone 3-β-hydroxylase	F3βH	*tt6*	3

Over-expression of the maize gene for CHS has been shown to complement the *Arabidopsis tt4* mutant, thereby restoring cyanidin synthesis and seed coat color (Dong *et al.*, *Plant Physiol.* 127:46-57, 2001). Complementation of these *Arabidopsis* mutants may therefore be employed to demonstrate the function of the inventive polynucleotides encoding enzymes involved in the tannin biosynthetic pathway.

Two chalcone synthase genes were identified from *F. arundinacea* (SEQ ID NO: 32 and 33). Sense constructs containing a polynucleotide including the coding region of one chalcone synthase gene, FaCHS2, (SEQ ID NO: 33) under the control of the CaMV 35S promoter were inserted into a binary vector and used to transform *Agrobacterium tumefaciens* LBA4404 using published methods (*see*, An G, Ebert PR, Mitra A, Ha SB, "Binary Vectors," *in* Gelvin SB, Schilperoort RA, eds., *Plant Molecular Biology Manual*, Kluwer Academic Publishers: Dordrecht, 1988). The presence and integrity of the binary

vector in *A. tumefaciens* was verified by polymerase chain reaction (PCR) using the forward primer provided in SEQ ID NO: 89 and reverse primer provided in SEQ ID: 90.

The *A. tumefaciens* containing the sense gene construct were used to transform *Arabidopsis tt4* mutants by floral dipping (Clough and Bent, *Plant J.* 16:735-743, 1998) and several independent transformed plant lines were established for the sense. Transformed plants containing the appropriate tannin gene construct were verified using PCR.

The presence of cyanidin in the transformed plants is demonstrated by a phenotypic change in plant seedling color and by analyzing cyanidin extracts made from transgenic plants grown under stressed conditions (Dong *et al.*, *Plant Physiol.* 127:46-57, 2001). Briefly, cyanidins are extracted from plant tissue with an acid/alcohol solution (HCl/methanol) and water. Chlorophyll is removed by freezing the extracts followed by centrifugation at 4 °C at 20,000 x *g* for 20 min. Any remaining chlorophyll is removed through a chloroform extraction. The absorbance at 530 nm is measured for each of the cyanidin extracts. Non-transgenic wild type and control *Arabidopsis* plants are used as controls.

Example 3

USE OF SUCROSE TRANSPORTERS TO COMPLEMENT A YEAST STRAIN UNABLE TO GROW ON SUCROSE

Two *Lolium perenne* genes, LpSUT2 (SEQ ID: 25) and LpSUT-like (SEQ ID: 27), and two *Festuca arundinacea* genes, FaSUT1 (SEQ ID NO: 22) and FaSUT2 (SEQ ID NO: 26) share amino acid sequence identity with sucrose transporter (SUT1 and SUT2) genes from other plant species (Barker *et al.*, *Plant Cell* 12:1153-1164, 2000; Weise *et al.*, *Plant Cell* 12:1345-1355, 2000; Lemoine, *Biochim. Biophys. Acta* 1465:246-262, 2000). The first plant gene encoding a sucrose carrier protein, from spinach, was isolated by functional expression in a yeast strain, SUSY7 (Riesmeier *et al.*, *EMBO J.* 11:4705-4713, 1992).

The gene of SEQ ID NO: 27 was digested and cloned into the yeast expression vector pYEP 112 A1 NE for functional complementation using this yeast system. Plasmid DNA was verified by sequencing and transformed into *S. cerevisiae* strain SUSY7, which had been

engineered to express cytosolic sucrose synthase enabling it to metabolize sucrose entering the cell. Constitutive expression of the grass sucrose transporters within this yeast strain facilitated transport of sucrose in to the cell and its growth on sucrose minimal media. Growth rates of recombinant and wild type yeast strains in both sucrose and glucose minimal media were observed.

Results showed that the yeast strain containing the gene of SEQ ID NO: 27 was able to grow on sucrose minimal medium because the constitutive expression of the SUT-like gene within this yeast strain facilitated transport of sucrose into the cell.

Example 4

USE OF ALKALINE/NEUTRAL INVERTASES TO CLEAVE SUCROSE

A number of *Lolium perenne* and *Festuca arundinacea* genes (SEQ ID NO: 5, 7 and 9-14) were identified that share amino acid sequence identity with alkaline/neutral invertase genes from other plant species (Sturm *et al.*, *Physiol. Planta* 107:159-165, 1999; Gallagher and Pollock, *J. Exp. Bot.* 49:789-795, 1998).

L. perenne gene AN_INV8 (SEQ ID NO: 12) was amplified by PCR from the start methionine using forward (SEQ ID NO: 91) and reverse (SEQ ID NO: 92) primers, then cloned into the pET41a expression plasmid. The resulting plasmid was transformed into *E. coli* BL21 cells using standard protocols, and protein expression induced using IPTG. The soluble recombinant protein was assayed for its ability to cleave sucrose. Cells were lysed in citrate buffer and the soluble protein incubated with 50mM sucrose in citrate buffer pH7. Reactions were terminated by boiling. Cleavage of the sucrose by neutral invertase activity was determined by the formation of glucose in this reaction. Levels of glucose were determined with a Glucose HK assay kit GAHK-20 (Sigma, St Louis MO) utilizing hexokinase coupled to glucose-6-phosphate dehydrogenase, and reduction of NAD measured by absorbance at 340nm.

Fig. 1 shows the invertase activity of recombinant AN_INV8 protein, measured as the amount (in μg) of glucose release from cleavage of sucrose per hour at pH7, and that of an empty vector (pET41a) control sample. The results showed that the purified protein released

35 μg of glucose per hour through the invertase cleavage of sucrose. No release was measured with the empty vector control.

Example 5

USE OF PYROPHOSPHATE-DEPENDENT PHOSPHOFRUCTOKINASE TO PHOSPHORYLATE FRUCTOSE-6-PHOSPHATE

Two *Lolium perenne* genes, LpPFPA (SEQ ID: 15) and LpPFPB (SEQ ID NO: 18), and two *Festuca arundinacea* genes, FaPFPA (SEQ ID NO: 16) and FaPFPB (SEQ ID NO: 19) share amino acid sequence identity with the A and B subunits of pyrophosphate-dependent phosphofructoskinase genes (PFP) from other plant species (Todd *et al.*, *Gene* 152:181-186, 1995; Carlisle *et al.*, *J. Biol. Chem.* 265:18366-18371, 1990) .

The entire coding regions were cloned into expression vector pBK-CMV, under the control of the CMV promoter for expression of recombinant protein in mammalian cells. The PFPA and PFPB genes from *Lolium perenne* or *Festuca arundinacea* were co-transfected in to mammalian HEK293T cells and protein extracted 48 hours later. Protein was also extracted from cells transfected with a negative control vector containing the β-galactosidase gene. Purified potato PFP (Sigma, St. Louis MO) was used as positive control. Activity of the PFP enzyme was measured spectrophotometrically by a decrease NADH and absorbance at 340 nm in a coupled reaction as described previously (Theodorou and Kruger, *Planta* 213:147-157, 2001). Briefly, the conversion of fructose-6-phosphate to fructose-1,6-diphosphate in the presence of activator, fructose-2,6-diphosphate was initiated by the addition of pyrophosphate and measured in a coupled reaction with aldolase, triose phosphate isomerase and glycerophosphate dehydrogenase.

Fig. 2 shows the PFP activity of the purified protein (conversion of fructose-6-phosphate to fructose-1-6-diphosphate) measured as conversion of PPi to inorganic phosphate. No conversion was obtained with the β-galactosidase negative control.

Example 6

USE OF SUCROSE PHOSPHATE SYNTHASE ENZYMES TO SYNTHESIZE SUCROSE

A *Lolium perenne* polynucleotide sequence (SEQ ID NO: 20) and a *F. arundinacea* polynucleotide sequence (SEQ ID NO: 21) have been identified that share identity with sucrose phosphate synthase (SPS) from other plant species. These genes are expressed in *E. coli* or *Pichia* using standard protocols, and the resulting purified protein assayed for its ability to synthesize sucrose from fructose-6-phosphate and uridine 5'-diphosphoglucose. Sucrose is detected by adding NAD and UDP-Glucose dehydrogenase, followed by the addition of anthrone reagent and then measuring the change in absorbance at 620 nm (Botha and Black, *Aust. J. Plant Physiol.* 27:81-85, 2000).

SEQ ID NOS: 1-88 are set out in the attached Sequence Listing. The codes for nucleotide sequences used in the attached Sequence Listing, including the symbol "n," conform to WIPO Standard ST.25 (1998), Appendix 2, Table 1.

All references cited herein, including patent references and non-patent publications, are hereby incorporated by reference in their entireties.

While in the foregoing specification this invention has been described in relation to certain preferred embodiments, and many details have been set forth for purposes of illustration, it will be apparent to those skilled in the art that the invention is susceptible to additional embodiments and that certain of the details described herein may be varied considerably without departing from the basic principles of the invention.

Claims

We claim:

1. An isolated polynucleotide comprising a sequence selected from the group consisting of: SEQ ID NO: 1-44.

2. An isolated polynucleotide comprising a sequence selected from the group consisting of:
   (a) complements of SEQ ID NO: 1-44;
   (b) reverse complements of SEQ ID NO: 1-44;
   (c) reverse sequences of SEQ ID NO: 1-44;
   (d) sequences that are 100-mers of a sequence of SEQ ID NO: 1-44;
   (e) sequences that are 40-mers of a sequence of SEQ ID NO: 1-44; and
   (f) sequences that are 20-mers of a sequence of SEQ ID NO: 1-44.

3. An isolated polynucleotide comprising a sequence selected from the group consisting of:
   (a) sequences having at least 75% identity to a sequence of SEQ ID NO: 1-44;
   (b) sequences having at least 90% identity to a sequence of SEQ ID NO: 1-44;
   (c) sequences having at least 95% identity to a sequence of SEQ ID NO: 1-44;
   (d) sequences having at least 98% identity to a sequence of SEQ ID NO: 1-44; and
   (e) sequences that hybridize to a sequence of SEQ ID NO: 1-44 under stringent hybridization conditions.

4. An isolated polypeptide encoded by a polynucleotide of any one of claims 1-3.

5. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of: SEQ ID NO: 45-88.

6. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of:

(a) sequences having at least 75% identity to a sequence of SEQ ID NO: 45-88;

(b) sequences having at least 90% identity to a sequence of SEQ ID NO: 45-88; and

(c) sequences having at least 95% identity to a sequence of SEQ ID NO: 45-88.

7. An isolated polynucleotide that encodes a polypeptide of any one of claims 5 and 6.

8. An isolated oligonucleotide probe or primer comprising at least 10 contiguous residues complementary to 10 contiguous residues of a nucleotide sequence recited in any one of claims 1-3.

9. A kit comprising a plurality of oligonucleotide probes or primers of claim 8.

10. A genetic construct comprising a polynucleotide of any one of claims 1-3.

11. A transgenic cell comprising a genetic construct according to claim 10.

12. A genetic construct comprising, in the 5'-3' direction:

(a) a gene promoter sequence;

(b) a polynucleotide sequence comprising at least one of the following: (1) a polynucleotide coding for at least a functional portion of a polypeptide of any one of claims 5 and 6; and (2) a polynucleotide comprising a non-coding region of a polynucleotide of any one of claims 1-3; and

(c) a gene termination sequence.

13. The genetic construct of claim 12, wherein the polynucleotide sequence is in a sense orientation.

14. The genetic construct of claim 12, wherein the polynucleotide is in an anti-sense orientation.

15. A transgenic plant cell comprising a genetic construct of claim 12.

16. A plant comprising a transgenic plant cell according to claim 12, or fruit or seeds or progeny thereof.

17. The plant of claim 16, wherein the plant is selected from the group consisting of: *Festuca arundinacea* and *Lolium perenne* species.

18. A method for modulating at least one of the fructan composition, cellulose, starch and tannin composition of a plant, comprising modulating the activity of a polypeptide of any one of claims 5 and 6 in the plant.

19. A method for modulating at least one of the fructan composition, cellulose composition, starch composition and tannin composition of a plant, comprising modulating the activity of a polynucleotide of any one of claims 1-3 in the plant.

20. The method of claim 19, comprising stably incorporating into the genome of the plant a polynucleotide of any one of claims 1-3.

21. The method of claim 19, comprising stably incorporating into the genome of the plant a genetic construct of any one of claims 10 and 12.

22. A method for producing a plant having at least one of altered fructan composition, altered cellulose composition, altered starch composition and altered tannin composition, comprising:

(a) transforming a plant cell with a genetic construct of any one of claims 10 and 12 to provide a transgenic cell; and

(b) cultivating the transgenic cell under conditions conducive to regeneration and mature plant growth.

23. A method for modifying the activity of a polypeptide involved in a fructan, cellulose, starch or tannin biosynthetic pathway in a plant, comprising modulating the activity of a polynucleotide of any one of claims 1-3 in the plant.

24. The method of claim 23, comprising stably incorporating into the genome of the plant a genetic construct of claim 12.

25. A method for modifying the activity of a polypeptide involved in a fructan, cellulose, starch or tannin biosynthetic pathway in a plant, comprising introducing into cells of the plant double stranded RNA corresponding to a polynucleotide of any one of claims 1-3, thereby inhibiting expression of a polypeptide encoded by the polynucleotide.

Fig. 1

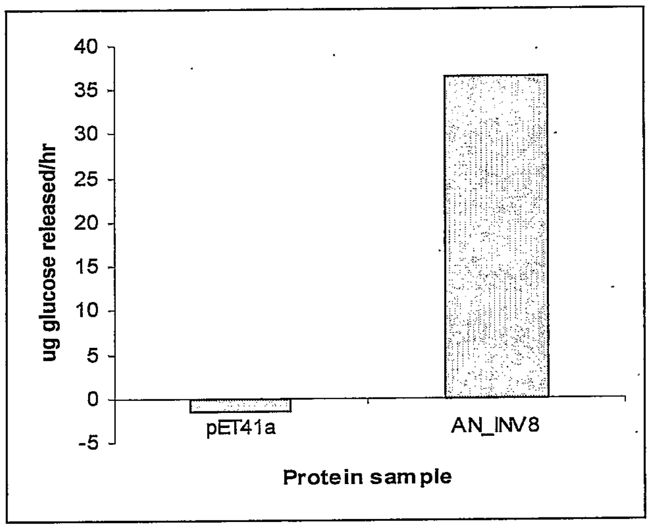
ug glucose released/hr
40
35
30
25
20
15
10
5
0
-5
pET41a
AN_INV8
Protein sample

Fig. 2

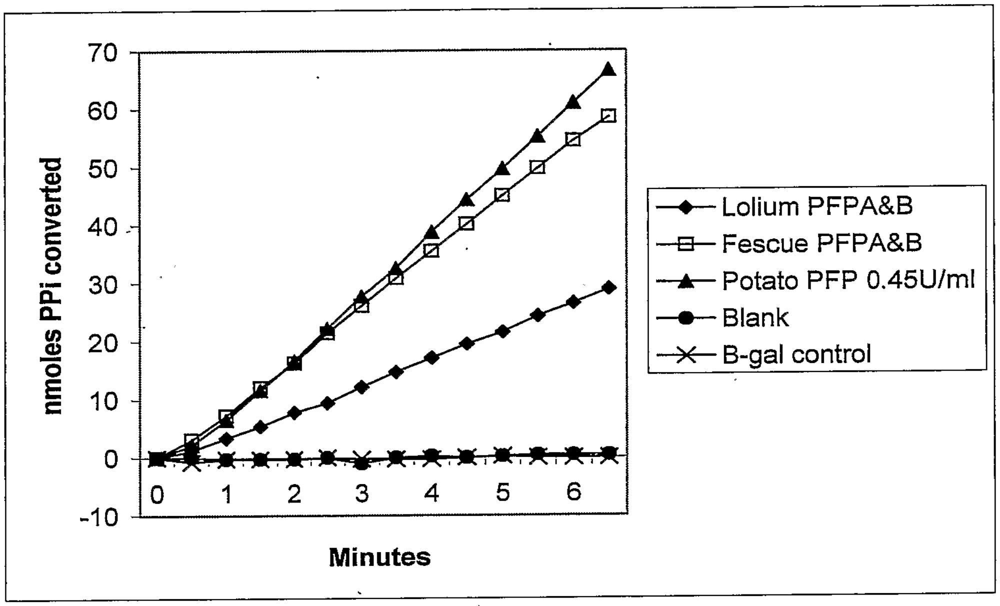
70
60
50
40
30
20
10
0
-10
nmoles PPi converted
0
1
2
3
4
5
6
Minutes
Lolium PFPA&B
Fescue PFPA&B
Potato PFP 0.45U/ml
Blank
B-gal control

Fig. 3

MAAAAVAPDAKIEKFRDAVAKLGEISENEKAGCISLVSRYLSGEAEQIEWSKIQTPTDEVVVPYDTLAPAP
EDLDAMKALLDKLVVLKLNGGLGTTMGCTGPKSVIEVRNGFTFLDLIVIQIESLNKKYGCDVPLLLMNSFN
THDDTQKIVEKYSNSNINIHTFNQSQYPRIVTEDFLPLPSKGQSGKDGWYPPGHGDVFPSLNNSGKLDTLL
SQGKEYVFVANSDNLGAIVDIKILNHLINNKNEYCMEVTPKTLADVKGGTLISYEGRVQLLEIAQVPDEHV
NEFKSIEKFKIFNTNNLWVNLKAIKRLVEADALKMEIIPNPKEVDGVKVLQLETAAGAAIRFFDNAIGING
PRSRFLPVKATSDLLLVQSDLYTLVDGYVIRNPARVKPSNPSIELGPEFKKVASFLARFKSIPSIVELDSL
KVSGDVSFGSGIVLKGNVTIAAKSGVKLEIPDGAVLENKDINGPEDL

Fig. 4

MAAVAADAKIEKFRDAVAKLDEISENEKAGCISLVSRYLSGEAEQIEWSKIQTPTDEVVVPYDTLAPAPQD
LDAMKALLDKLVVLKLNGGLGTTMGCTGPKSVIEVRNGFTFLDLIVIQIESLNKKYGCDVPLLLMNSFNTH
DDTQKIVEKYSNSNINIHTFNQSQYPRIVTEDFLPLPSKGKSGKDGWYPPGHGDVFPSLNNSGKLDTLLSQ
GKEYVFVANSDNLGAIVDIKILNHLINNQNEYCMEVTPKTLADVKGGTLISYEGRVQLLEIAQVPDEHVNE
FKSIEKFKIFNTNNLWVNLKAIKRLVEADALKMEIIPNPKEVDGVKVLQLETAAGAAIRFFEKAIGINGPR
SRFLPVKATSDLLLVQSDLYTLVDGYVIRNPARVKPSNPSIELGPEFKKVASFLARFKSIPSIVELDSLKV
SGDVTFGSGVVLKGNVTIAAKSGVKLEIPDGAVLENKDINGPEDL

Fig. 5

CLRRRTYSNSGDTHADPNGPVYYGGWYHLFYQHNPYGDSWGNVSWGHAVSKDLVNWRHLPVALVPDQWYDI
NGVLTGSITVLPDGRVILLYTGNTDTFSQVQCLAVPADPSDPLLRSWIKHPANPILFPPPGIGLKDFRDPL
TAWFEHSDNTWRTIIGSKDDDGHAGIVLSYKTTDFVNYELMPGNMHRGPDGTGMYECLDIYPVGGNSSEML
GGDSSPEVLFVLKESANDEWHDYYALGWFDATANTWTPQDPEADLGIGLRYDWGKYYASKSFYDPIKNRRV
VWAFVGETDSEQADKAKGWASLMSIPRMVELDKKTRTNLIQWPVEEIETLRRNVTDLGGITVEAGSVIHLP
LQQGGQLDIEASFRLNSSDIDALNEADVGFNCSSSAGAAVRGALGPFGLLVFADGRHEQTAAYFYVSKGLD
GSLLTHYCHDESRSTRAKDVVSRVVGGTVPVLDGETFSVRVLVDHSIVQSFVMGGRTTVTSRAYPTEAIYA
AAGVYLFNNATSATITAEGLVVYEMASAESQAFLADDM

Fig. 6

MESSAVVVPGTTAPLLPYDSRENQSSGGGVWWRACAASAVVLLVVVGFFAGGRVDLGQAGEVSATSSVPAA
MMEIPRSRGKNFGVSEKADGGFPWSNAMLQWQHTGFHFQPLKHYMNDPNGPVYYGGWYHLFYQHNPYGDSW
GNVSWGHAVSKDLVNWRHLPVALVPDQWYDINGVLTGSITVLPDGRVILLYTGNTDTFSQVQCLAVPADPS
DPLLRSWIKHPANPILFPPPGIGLKDFRDPLTAWFEHSDNTWRTIIGSKDDDGHAGIVLSYKTTDFVNYEL
MPGNMHRGPDGTGMYECLDIYPVGGNSSEMLGGDSSPEVLFVLKESANDEWHDYYALGWFDATANTWTPQD
PEADLGIGLRYDWGKYYASKSFYDPIKNRRVVWAFVGETDSEQADKAKGWASLMSIPRMVELDKKTRTNLI
QWPVEEIETLRRNVTDLGGITVEAGSVIHLPLQQGGQLDIEASFRLNSSDIDALNEADVGFNCSSSAGAAV
RGALGPFGLLVFADGRHEQTAAYFYVSKGLDGSLLTHYCHDESRSTRAKDVVSRVVGGTVPVLDGETFSVR
VLVDHSIVQSFVMGGRTTVTSRAYPTEAIYAAAGVYLFNNATSATITAEGLVVYEMASAESQAFLADDM

Fig. 7

MAIAAAAALLPLHLGCSDAAPRRPGNSLRAHLRKGGIRGRRRSPPCAVNSLHPSGNPKTPGGGDVGGAWGL
NGGATAKPDHAPPSQRRRAPRDVEEEAWALLRESVVSYCGSPVGTIAACDPNDASPLNYDQVFIRDFVPSG
VAFLLKGEHEIVRNFILHTLQLQSWEKTIDCHSPGQGLMPASFKVRVVPLDGGDDGATEEVLDPDFGEAAI
GRVAPVDSGLWWIILLRAYGKCSGDLSFHERVDVQTGIKLILKLCLADGFDMFPTLLVTDGSCMMDRRMGI
HGHPLEIQALFYSALLSAREMLTPEDGSADLIRALNSRLMALSFHIREYYWLEKRKLNEIYRYKTEEYSYD
AVNKFNIYPDQIPPWLVEWIPPKGGYFIGNLQPAHMDFRFFSLGNLWSIVSSLATADQSHAILDLVEAKWS
DLVAEMPMKICYPALEDQEWKFITGSDPKNTPWSYHNGGSWPTLLWQLTVACIKMNRPEIAARAVEVAESR
ISMDKWPEYYDTKRGRFIGKQARLFQTWSIAGFLVAKLLLENPEKSRILWNNEDEEILNALSLMTGPSSPK
RKRGRKTYIV

Fig. 8

MNGQTTMGLAAAAAAAVRPCRRRLLSSASAAAAAKASATPLFPRCSHPQHQQHSRRIPFLVSAASHTSQSD
PSTTPTPVTSDPRSAVAGNLPFFDRVLFPGSFPLETPPVEEPAPAPPADEAQASASPVREESDTEREAWRL
LRRAVVSYCGDPVGTVAAEDPECTEMLNYDQVFIRDFVPSALAFLMRGETEIVRNFLLHTLQLQSWEKTVD
CYSPGQGLMPASFKIKTVPLDENNEAFEEVLDPDFGESAIGRVAPVDSGLWWIILLRAYCKFTGDYSLQER
VDVQTGIKLILSLCLTDGFDMFPTLLVTDGSCMIDRRMGIHGHPLEIQALFYSALRCSREMIVMNDGSKHL
LQAINNRLSALSFHIREYYWVDMKKINEIYRYKTEEYSHDATNKFNIYPEQIPSWLVDWVPEKGGYLIGNL
QPAHMDFRFFSLGNLWAISSSLTTPTQAEGILSLIEEKWDDLVANMPLKICYPAMEDDEWRIVTGSDPKNT
PWSYHNGGSWPTLLWQFTLACIKMGRPELARRAIAVAEEKLSADKWPEYYDTRSGRFVGKQSRSYQTWTIA
GFLTSKILLENPELASILTCDEDLELLEGCACCLSKRTRCSRRVTKSDIIG

Fig. 9

MAIAAAAALLPLHLGCSDAAPRRPGNSLRAHLRKGGIRGRRRSPPCAVNSLHPSGNPKTPGGGDVGGGRGV
NGGATAKPDHAPPSQRRRAPRDVEEEAWALLRESVVSYCGSPVGTIAACDPNDASPLNYDQVFIRDFVPSG
VAFLLKGEHEIVRNFILHTLQLQSWEKTIDCHSPGQGLMPASFKVRVVPLDGGDDGATEEVLDPDFGEAAI
GRVAPVDSGLWWIILLRAYGKCSGDLSFHERVDVQTGIKLILKLCLADGFDMFPTLLVTDGSCMMDRRMGI
HGHPLEIQALFYSALLSAREMLTPEDGSADLIRALNSRLMALSFHIREYYWLEKRKLNEIYRYKTEEYSYD
AVNKFNIYPDQIPPWLVEWIPPKGGYFIGNLQPAHMDFRFFSLGNLWSIVSSLATADQSHAILDLVEAKWS
DLVAEMPMKICYPALEDQEWKFITGSDPKNTPWSYHNGGSWPTLLWQLTVACIKMNRPEIAARAVEVAESR
ISTDKWPEYYDTKRGRFIGKQARLFQTWSIAGFLVAKLLLENPEKSRILWNNEDEEILNALSLMTGPSSPK
RKRGRKTYIV

Fig. 10

MKRVSSHVSIASEAEINLDLSRLLIDKPRYTLERKRSFDEQSWSELTHTHRQNDGFDSVLQSPAFRTGFDS
PFSMGTHFGEPSGPHPLVNEAWEALRKSVVYFRGQPVGTIAAVDHASEEVLNYDQVFVRDFVPSALAFLMN
NEPEIVKNFLLKTLHLQSSEKMVDRFKLGAGAMPASFKVDRNKSRNTETLVADFGESAIGRVAPVDSGFWW
IILLRAYTKYTGDASLSESPDCQKCMRLILNLCLSEGFDTFPTLLCTDGCSMIDRRMGIYGYPIEIQALFY
MALRCALQMLKPDGEGKDFIEKIGQRLHALTYHMRNYFWLDFPHLNNIYRYKTEEYSHTAVNKFNVIPDSI
PDWVFDFMPCRGGYFLGNVSPAMMDFRWFALGNCIAIISSLATPEQSSAIMDLIEERWDELVGEVPLKICY
PAIENHEWRIITGCDPKNTRWSYHNGGSWPVLLWLLTAACIKTGRPQMAKRAIELSEARLLKDGWPEYYDG
KLGKFVGKQARKFQTWSIAGYLVARMMLEDPSTLMMISMEEDRPVKPTMRRSASWNA

Fig. 11

MEAPGGGAGPMPTTPSHASIADSDDFDLSRLLNHRPRINVERQRSFDDRSLGDLYLSAMDSRGGYMDSYDS
MYSPGGGLRSLTGTPASSTRLSFEPQLLVAEAWEALRRSLVCFRGEPLGTIAAVDSSSDEVLNYDQVFVRD
FVPSALAFLMNGEPDIVKNFLLKTLLLQGWEKRIDRFKLGEGAMPASFKVLKDPKRGVDTLAADFGESAIG
RVAPADSGFWWIILLRAYTKSTGDLTLAETPECQKGIRLIMNQCLAEGFDTFPTLLCADGCCMIDRRMGVY
GYPIEIQALFFMSLRCALLLLKPAVEGNSSSKDDDIMERIVTRLHALSYHMRSYFWLDFQQLNVIYRFKTE
EYSHTAVNKFNVIPESIPDWLFDFMPSRGGYFVGNVSPARMDFRWFALGNCVAILASLATPEQAGAIMDLI
EERWEDLIGEMPLKICYPTIEGHEWQNVTGCDPKNTRWSYHNGGSWPVLIWLLTAACIKTGRLKIARRAID
LAEARLGKDGWPEYYDGKLGRYVGKQARKHQTWSIAGYLVAKMMLEDPSHLGMIS

Fig. 12

MEFGAPGGMRRSASHNSLSGSDDFDLTHLLNKPRINVERQRSFDDRSLSDVSYSGGGHARGAGGGFDGMYS
PGGGLRSLVGTPASSALHSFEPHPIVGDAWEALRRSLVFFRGQPLGTIAAYDHASEEVLNYDQVFVRDFVP
SAMAFLMNGEPEIVKNFLLKTVLLQGWEKKVDRFKLGEGAMPASFKVLHDDKKGVDTLHADFGESAIGRVA
PVDSGFWWIILLRAYTKSTGDLTLAEKPECQKAMRLILSLCLSEGFDTFPTLLCADGCCMIDRRMGVYGYP
IEIQSLFFMALRCALLMLKHDNEGKDFVERIATRLHALSYHMRSYFWLDFQQLNDIYRYKTEEYSHTAVNK
FNVIPDSIPDWLFDFMPCEGGFFVGNVSPARMDFRWFALGNMIAIVSSLATPEQSTAIMDLIEERWEELIG
EMPLKICYPAIENHEWRIVTGCDPKNTRWSYHNGGSWPVLLWLLTAASIKTGRPQIARRAIDLAERRLLKD
GWPEYYDGKLGKYVGKQARKFQTWSIAGYLVAKMLLEDPSHLGMIALEEDKAMKPVLRRSASWTN

Fig. 13

MDSDYGVPRELSEVQKKRTLYQPDLPPCLQGTTVRVEYGDVAIAADPAGAHVISHAFPHTYGQPLAHFLRK
AANVADAKVISEHPAVRVGIVFCGRQSPGGHNVIWGLHDAIKAHNPNSKLIGFLGGSDGLLAQKTLEITDE
VLSSYKNQGGYDMLGRTKDQIRTTEQVNGAMASCQALKLDALIIIGGVTSNTDAAQLAETFAEAKCATKVV
GVPVTLNGDLKNQFVETTVGFDTICKVNSQLISNMCTDALSAEKYYYFIRMMGRKASHVALECALQSHPNM
VILGEEVAASKLTIFDITKQICDAVQARAEKDKNHGVILIPEGLVESIPELYALLQEINGLHGKGVSIENI
SSQLSPWASALFEFLPQFIRQQLLLRPESDDSAQLSQIETEKLLAQLVETEMNKRLKEGTYKGKKFNAICH
FFGYQARGAMPSKFDCDYAYVLGHVSYHILAAGLNGYMATVTNLKSPLNKWRCGAAPISSMMTVKRWSRGP
STTQIGKPAVHMASVDLRGKAYELLRQNSSSCLLEDIYRNPGPLQFEGPGSDSKPISLCVEDQDYMGRIKK
LQEYLEKVKSIVKPGCSQDVLKAALSAMSSVTDTLAIMTSSSTGQAPL

Fig. 14

MDSDYGVPRELSEVQKKRTLYQPELPPCLQGTTVRVEYGDVAIAADPAGAHVISHAFPHTYGQPLAHFLRK
AANVADAKVISEHPAVRVGIVFCGRQSPGGHNVIWGLHDAIKAHNSNSKLIGFLGGSDGLLAQKTLEITDE
VLSSYKNQGGYDMLGRTKDQIRTTEQVNGAMASCQDLKLDALIIIGGVTSNTDAAQLAETFAEAKCATKVV
GVPVTLNGDLKNQFVETTVGFDTICKVNSQLISNMCTDALSAEKYYYFIRMMGRKASHVALECALQSHPNM
VILGEEVAASKLTIFDITKQICDAVQARAEKDKNHGVILIPEGLVESIPELYALLQEINGLHGKGVSIENI
SSQLSPWASALFEFLPQFIRHQLLLRPESDDSAQLSQIETEKLLAQLVETEMNKRLKEGTYKGKKFNAICH
FFGYQARGAMPSKFDCDYAYVLGHVSYHILAAGLNGYMATVTNLKSPLNKWRCGAAPISSMMTVKRWSRGP
STTQIGKPAMHMATVDLRGKAYELLRQNSSSYLLEDIYRNPGPLQFEGPGADSKPISLCVEDQDYMGRIKK
LQEYLEKVKSIVKPGCSQDVLKAALSAMSSVTETLAIMTSSSTGQAPL

Fig. 15

MAAAAVATSNGASANGPTPGRLASVYSEVQTSRIAHALPLPSVLRSHFTLADGAASSATGNPEEIAKLFPN
LYGQPSAAVVPSAQPVATKPLKIGVVLSGGQAPGGHNVICGIFDYLQERAKGSTMYGFKGGPAGVMKGKYV
ELNADFVYPYRNQGGFDMICSGRDKIETPEQFKQAEDTVTKLDLDGLVVIGGDDSNTNACLLGEYFRGRNL
KTRVIGCPKTIDGDLKCKEVPTSFGFDTACKIYSEMIGNVMTDARSTGKYYHFVRLMGRAASHITLECALQ
THPNVSLIGEEVAEKKETLKQVTDYITDVICKRAELGYNYGVILIPEGLIDFIPEVQKLIAELNEILAHDV
VDEAGAWKSKLQPESRQLFDFLPNTIQEQLLLERDPHGNVQVAKIETEKMLIAMVETELEKRRSAGKYSAH
FRGQSHFFGYEGRCGLPTNFDSSYCYALGYGAGALLQFGKTGLISSVGNLAAPVEEWTVGGTPLTALMDVE
RRHGKFKPVIKKAMVELDAAPFKKFASMRDEWAIKNRYISPGPIQFSGPGSDASNHTLMLELGAQT

Fig. 16

MAAAAVATSNGASANGPTPGRLASVYSEVQTSRIAHALPLPSVLRSHFTLADGAASSATGNPEEIAKLFPN
LYGQPSAAVVPSAQPVATKPLKIGVVLSGGQAPGGHNVICGIFDYLQERAKGSTMYGFKGGPAGVMKGKYV
ELNADFVYPYRNQGGFDMICSGRDKIETPEQFKQAEDTVTKLDLDGLVVIGGDDSNTNACLLGEYFRGRNL
KTRVIGCPKTIDGDLKCKEVPTSFGFDTACKIYSEMIGNVMTDARSTGKYYHFVRLMGRAASHITLECALQ
THPNVSLIGEEVAEKKETLKQVTDYITDVICKRAELGYNYGVILIPEGLIDFIPEVQKLIAELNEILAHDV
VDEAGAWKSKLQPESRQLFDFLPNTIQEQLLLERDPHGNVQVAKIETEKMLIAMVETELEKRRSAGKYSAH
FRGQSHFFGYEGRCGLPTNFDSSYCYALGYGAGALLQFGKTGLISSVGNLAAPVEEWTVGGTPLTALMDVE
RRHGKFKPVIKKAMVELDAAPFKKFASMRDEWAIKNRYISPGPIQFSGPGSDASNHTLMLELGAQT

Fig. 17

MAAAAVATSNGASANGPTPGRLASVYSEVQTSRIAHALPLPSVLRSNFTLADGPASSATGNPEEIAKLFPN
LYGQPSAAVVPSAEPVPTKPLKIGVVLSGGQAPGGHNVICGIFDYLQERAKGSTMYGFKGGPAGIMKGKYI
ELNADFVYPYRNQGGFDMICSGRDKIETPEQFKQAEDTVNKLDLDGLVVIGGDDSNTNACLLGEYFRGRNL
KTRVIGCPKTIDGDLKCKEVPISFGFDTACKIYSEMIGNVMTDARSTGKYYHFVRLMGRAASHITLECALQ
THPNVSLIGEEVAEKKETLKQVTDYITDVICKRAELGYNYGVILIPEGLIDFIPEVQKLIAELNEILAHDV
VDEAGAWKSKLQPESRQLFDFLPNTIQEQLLLERDPHGNVQVAKIETEKMLIAMVETELEKRRAAGKYSAH
FRGQSHFFGYEGRCGLPTNFDSSYCYALGYGAGALLQFGKTGLISSVGNLAAPVEEWTVGGTPLTALMDVE
RRHGKFKPVIKKAMVELDAAPFKKFASMRDEWAIKNRYISPGPIQFSGPGSDASNHTLMLELGAQI

Fig. 18

MVGNDNWINSYLDAILDAGKSSIGGDRPSLLLRERGHFSPARYFVEEVITGYDETDLYKTWLRANAMRSPQ
ERNTRLENMTWRIWNLARKKKELEKEEACRLLKRHPETEKTRTDATADMSEDLFDGEKGEDAGDPSVAYGD
STTGSSPKTSSVDKLYIVLISLHGLVRGENMELGRDSDTGGQVKYVVEFAKALSSSPGVYRVDLLTRQIVA
PNFDRSYGEPEEMLVSTTFKNSKHERGVNSGGYIIRIPFGPKDKYLAKEHMWPFIQDFVDGALSHILRMSK
TIGEEIGCGHPVWPAVIHGHYASAGVAAALLSGALNLPMAFTGHFLGKDKLEGLLKQGRQSREQINMTYKI
MRRIEAEELSLDASEIVIASTRQEIEEQWNLYDGFEVILARKLRARVKRGANCYGRYMPRMVIIPPGVEFG
HVVHDFDMDGEEENHGPASEDPPIWSQIMRFFTNPRKPMILAVARPYPEKNITSLVKAFGECRPLRELANL
TLIMGNREAISKMHNTSASVLTSVLTLIDEYDLYGQVAYPKHHKHSEVPDIYRLATRTKGAFVNVAYFEQF
GVTLIEAAMNGLPVIATKNGAPVEINQVLNNGLLVDPHDQNAIADALYKLLSEKQLWSRCRENGLKNIHQF
SWPEHCKNHLSRILTLGARSPAIGSKEERSNAPISGRKHIIVISVDSVNKEDLVRIIRNAIEAAHTQNTPA
STGFVLSTSLTLSEICSLLVSVGMHPAGFDAFICNSGSSIYYPSYSGNTPSSSKVTHVIDQNHQSHIEYRW
GGEGLRKYLVKWATSVVERKGRIERQMIFEDSEHSSTYCLAFKVVNPNHLPPLKELRKLMRIQSLRCNALY
NHSATRLSVTPIHASRSQAIRYLFIRWGIELPNIVVLVGESGDSDYEELLGGLHRTIILKGDFNIAANRIH
TVRRYPLQDVVALDSSNIIEVEGCTTDVIKSALRQIGVPTQ

Fig. 19

MVGGMCGNDNWINSYLDAILDAGKGAPGGGAGPGGGRGGGGGGAGDRPSLLLRERGHFSPARYFVEEVITG
YDETDLYKTWSRANAMRSPQERNTRLENMTWRIWNLARKKKEXEAEEANRLLKRRLETEKPRTDAAAEMSE
DLFEGQKGEDAGDASVAYGDSSASNTPRISSIDKLYIVLISLHGLVRGENMELGRDSDTSGQVKYVVELAK
ALSSCPGVYRVDLLTRQILAPNYDRGYGEPSETLLPTNLKNFKHERGENSGAYITRIPFGPKDKYLAKEQL
WPYVQEFVDGALSHIVRMSKTIGEEIGCGHPMWPAAIHGHYASAGVAAALLSGALNVHMIFTGHFLGRDKL
EGLLKQGKQTREEINMTYKIMRRIEAEELSLDASEIVIASTRQEIEEQWNLYDGFEVMLARKLRARVKRGA
NCYGRYMPRMVIIPPGVEFGHMIQDFDMDGEEDSPSPASEDPPIWSEIMRFFTNPRKPLILAVARPYPEKN
ITTLVRAFGECRPLRELANLTLIMGNREAISKMSNMSAAVLTSVLTLIDEYDLYGQVAYPKHHKHSEVLDI
YRLAARTKGAFVNVAYFEQFGVTLIEAAMHGLPVIATKNGAPVEIHQVLNNGLLVDPHDQNAIADALYKLL
SEKQLWSRCRENGLKNIHQFSWPEHCKNYLSRILTLSPRYPAFASNDDQIKAPIKGRKYIIVIAVDSASKK
DLAFIIRNSIEATRTETSSGSTGFVLSTSLTISEIHSLLISAGMVPTDFDAFICNSGSDLFYPSQTGDSPS
TSRVTFALDRNYQSRVEYHWGGEGLRKYLVKWASSVVERRGRMEKQVIFDDSEHSSTCCLAFRVVNPNYLP
PLKELQKLMRVQSLRCHALYNHSATRLSVIPIHASRSQAIRYLSVRWGIELPNVVILVGESGDSDYEELFG
GLHKTVVLNGEFNTPANRIHTVRRYPLQDVIALDCSNIVGVQGCSTDCMRSTLEKLGIPTK

Fig. 20

MVRGGGNGEVELSVGAGGGGGGAGGLVEPPVPISLGRLVLAGMVAGGVQYGWALQLSLLTPYVQTLGLSHA
LTSFMWLCGPIAGLVVQPCVGLYSDKCTSRWGRRRPFIMTGCVLICIAVVIVGFSADIGAALGDSKEECSL
YHGPRWHAAIVYVLGFWLLDFSNNTVQGPARALMADLSGKYGPSAANSIFCSWMALGNILGYSSGSTDKWH
KWFPFLRTRACCEACANLKGAFLVAVLFLCMCLVITLIFAKEVPYKRIAPLPTKANGQVEVEPSGPLAVFQ
GIRNLPSGMPSVLLVTGLTWLSWFPFILYDTDWMGREIYHGDPKGTPAEMSAFQDGVRAGAFGLLLNSIIL
GFSSFLIEPMCKRLGPRVVWVSSNFLVCIAMAATAIISWWSTKEFHEYVQHAITASKDIKIVCMALFAFLG
VPLAILYSVPFAVTAQLAASKGGGQGLCTGVLNISIVIPQVIIALGAGPWDQLFGKGNIPAFAAASAFALI
GGIVGIFLLPKISRRSFRAVSTGGH

Fig. 21

ICVAVVVVGFSADIGAALGDSKEECSLYHGPRWHAAIVYVLGFWLLDFSNNTVQGPARALMADLSGKYGPS
AANSIFCSWMALGNILGYSSGSTDKWHKWFPFLRTRACCEACANLKGAFLVAVLFLCFCLVITLIFAKEVP
YKRIAPLPTKANGQVEVEPSGPLAVFQGFRNLPSGMPSVLLVTGLTWLSWFPFILYDTDWMGREIYHGDPK
GTPAEASAFQDGVRAGAFGLLLNSIILGFSSFLIEPMCKRLGPRVVWVSSNLLVCIAMAATAIISWWSTKE
FHEYVQHAITASKDIKIVCMVLFAFLGVPLAILYSVPFAVTAQLAANKGGGQGLCTGVLNISIVIPQVIIA
LGAGPWDQLFGKGNIPAFAAASAFALIGGIVGIFLLPKISRHSFRAVSTGGH

Fig. 22

MVRGGGNSEVELSVGAGGGGGGAGGLVEPPVPISLGRLVFAGMVAGGVQYGWALQLSLLTPYVQTLGLSHA
LTSFMWLCGPIAGLVVQPCVGLYSDKCTSRWGRRRPFIMTGCVLICIAVVIVGFSADIGAALGDSKEECSL
YHGPRWHAAIVYVLGFWLLDFSNNTVQGPARALMADLSGKYGPSAANSIFCSWMALGNILGYSSGSTDKWH
KWFPFLRTRACCEACANLKGAFLVAVLFLCFCLVITLIFAKEVPYKRIAPLPTKANGQVEVEPSGPLAVFQ
GFRNLPSGMPSVLLVTGLTWLSWFPFILYDTDWMGREIYHGDPKGTPAEASAFQDGVRAGAFGLLLNSIIL
GFSSFLIEPMCKRLGPRVVWVSSNLLVCIAMAATAIISWWSTKEFHEYVQHAITASKDIKIVCMVLFAFLG
VPLAILYSVPFAVTAQLAANKGGGQGLCTGVLNISIVIPQVIIALGAGPWDQLFGKGNIPAFAAASAFALI
GGIVGIFLLPKISRHSFRAVSTGGH

Fig. 23

MPPPRRPTTGGTTTTSAALPPPRKVPLRSLLRAASVACGVQFGWALQLSLLTPYVQELGIPHAFASLVWLC
GPLSGLLVQPLIGHLSDRIAPADSPLGRRRPFIAAGAASIAFSVLTVGFSADLGRLFGDNVRPGSTRYGAI
IVYMIGFWLLDVGNNATQGPCRAFLADLTENDPRRTRIANAYFSLFMALGNILGYATGAYSGWYKIFPFTI
TESCGVSCANLKSAFLLDIIILAITTYVTVVTVQDNPTFGSDEAAPRPSSHEEEAFLFELFGSFKYFTMPV
WMVLIVTSLTWIGWFPFILFDTDWMGREIYRGSPEIVADTQKYHDGVRMGSFGLMLNSVLLGITSVVTEKL
CRKWGAGLVWGVSNIIMALCFVAMLVITYVAQNLDYGPSGAPPTGIVVASLTVFTILGAPLSITYSIPYAM
ATSRVENLGLGQGLAMGILNLSIVIPQIIVSLGSGPWDSLFGGGNAPSFWVAAAASFIGGLVAILGLPRAR
IAPKKRSQR

Fig. 24

MPPPRRPNAGGTTSAPLPPPRKVPLRSLLRAASVACGVQFGWALQLSLLTPYVQELGIPHAFASLVWLCGP
LSGLLVQPLIGHLSDRIAPADSPLGRRRPFIAAGAASIAFSVLTVGFSADLGRLFGDNIRPGSTRFGAIIV
YMIGFWLLDVGNNATQGPCRAFLADLTENDPRRTRIANAYFSLFMALGNILGYATGAYSGWYKIFPFTITE
SCGVSCANLKSAFLLDIIILAITTYVTVVTVQDNPTFGSDEAAPRPSSHEEEAFLFELFGSFKYFTLPVWM
VLIVTSLTWIGWFPFILFDTDWMGREIYRGSPEIVADTQKYHDGVRMGSFGLMLNSVLLGITSVVMEKLCR
KWGAGLVWGVSNIIMALCFVAMLIITYVAKNLDYGPSGAPPTGIVVASLAVFTILGAPLSITYSIPYAMAT
SRVENLGLGQGLAMGILNLSIVIPQIIVSLGSGPWDSLFGGGNAPSFWVAAAASFIGGLVAILGLPRARIA
PKKRSQR

Fig. 25

MVDQDHDGRRRQEEATAVAASSVPLLEKKPGDVPYYVEGCPGCAVDRRKATDPGIPYGSFIYIWVVILCTA
IPISSLFPFLYFMIRDLHIAERTEDIGFYAGFVGAAFMFGRCLTSTIWGIAADRIGRKPVVIFGVFSVVIF
NALFGLSVTYWMAIATRFLLGALNGLLGPMKAYAIEVCRPEHEALALSLVSTAWGIGLIIGPALGGYLALP
AEKYPNIFSPDSLFGRFPYFLPCLCTSVFAAAVLIGCIWMPETLHKHKVNENRNQSVESLEAHLIDPKEKV
EQSNSPDTKKSLFKNWPLMSSIIVYCVFSFHDMAYTEVFSLWAESDRTYGGLSLSSEDVGQTLAITGSSLL
VYQLFLYPRINRVLGPIKSSQIAAGICIPILFAYPYMTYLSEPGLSIVLNIASVIKNNLGVTIITGTFILQ
NNAVPQDQRGAANGLAMTGMSFFKAVAPAGAGIVFSWAQKRQHAFFFPGDQMVFFLLNIIELLGLLLTFKF
FLAVPDKSDSN

Fig. 26

MSSMQFSSVLPLEGKACVCPVRSANNGCERLKVGDSSSLRHEMALRRKCNGARGGGAADGAQCVLTSDASP
DTLVVRSSFRMNYADPNEVAAVILGGGTGTQLFPLTSTRATPAVPIGGCYRLIDIPMSNCFNSGINKIFVM
TQFNSASLNRHIHRTYLGGGINFTDGSVEVLAATQMPGEAAGWFRGTADAVRKFIWVLEDYYKHKSIEHIL
ILSGDQLYRMDYMELVQKHVDDNADITLSCAPVGESRASEYGLVKFDSSGRVIQFSEKPKGADLEAMKVDT
SFLNFAIDDPAKNPY-IASMGVYVFKREVLLNLLKSRYTELHDFGSEILPRALHDHNVQAYVFTDYWEDIGT
IRSFFDANMALCEQPPKFEFYDPKTPFFTSPRYLPPTKSDKCRIKEAIISHGCFLRECTIEHSIIGVRSRL
NSGSVLKNAMMMGADLYETEDEISGLLSEGKVPIGVGENSKLSNCIIDMNARIGRDVVIANSEGVQEADRP
EEGYYIRSGIVVILKNATVKDGTVV

Fig. 27

MSSMQFSSVLPLEGKACVCPVRSANNGCERLKVGDSSSLRHEMALRRKCNGARGGGAADGAQCVLTSDASP
DTLVVRSSFRMNYADPNEVA**AVILGGGTGTQLFPLTSTRATPAVPIGGCYRLIDIPMSNCFNSGINKIFVM**
TQFNSASLNRHIHRTYLGGGINFTDGSVEVLAATQMPGEAAGWFRGTADAVRKFIWVLEDYYKHKSIEHIL
ILSGDQLYRMDYMELVQKHVDDNADITLSCAPVGESRASEYGLVKFDSSGRVIQFSEKPKGADLEAMKVDT
SFLNFAIDDPAKNPYIASMGVYVFKREVLLNLLKSRYTELHDFGSEILPRALHDHNVQAYVFTDYWEDIGT
IRSFFDANMALCEQPPKFEFYDPKTPFFTSPRYLPPTKSDKCRIKEAIISHGCFLRECTIEHSIIGVRSRL
NSGSVLKNAMMMGADLYETEDEISGLLSEGKVPIGVGENSKLSNCIIDMNARIGRDVVIANSEGVQEADRP
EEGYYIRSGIVVILKNATVKDGTVV

Fig. 28

MTGAPPSTVMAMGAATSPCKILSATQRASTAAASASTSRESVSLRAPRGRRQRPRPRGLALSLAPARRPFV
FSPRAVSDSKSSQTCLDPDASTS**VLGIILGGGAGTRLYPLTKKRAKPAVPLGANYRLIDIPVSNCLNSNIS**
KIYVLTQFNSASLNRHLSRAYGSNIGGYKNEGFVEVLAAQQSPDNPNWFQGTADAVRQYLWLFEEHNVMEY
LILAGDHLYRMDYEKFIQAHRETDADITVAALPMDEERATAFGLMKIDEEGRIVEFAEKPKGEQLKAMMVD
TTILGLDDVRAKEMPYIASMGIYVISKHVMLQLLRDQFPGANDFGSEVIPGATSTGMRVQAYLYDGYWEDI
GTIEAFYNANLGITKKPIPDFSFYDRSAPIYTQPRHLPPSKVLDADVTDSVIGEGCVIKNCKIHHSVVGLR
SCISEGAIIEDTLLMGADYYETEADKKLLADKGGIPIGIGKNSHIRRAIIDKNARIGDNVKIINVDNVQEA
ARETDGYFIKSGIVTVIKDALLPSGTVI

Fig. 29

MTRAPPSTVMAMGAATSPCKILSATQRASAAAPSASTSRESVCLLRAPRGRRQRPRGLALSLAPARRPFVF
SPRAVSDSKSSQTCLDPDASTSVLGIILGGGAGTRLYPLTKKRAKPAVPLGANYRLIDIPVSNCLNSNISK
IYVLTQFNSASLNRHLSRAYGSNIGGYKNEGFVEVLAAQQSPDNPNWFQGTADAVRQYLWLFEEHNVMEYL
ILAGDHLYRMDYEKFIQAHRETDADITVAALPMDEERATAFGLMKIDEEGRIVEFAEKPKGEQLKAMMVDT
TILGLDDVRAKEMPYIASMGIYVISKHVMLQLLRDQFPGANDFGSEVIPGATSTGMRVQAYLYDGYWEDIG
TIEAFYNANLGITKKPIPDFSFYDRSAPIYTQPRHLPPSKVLDADVTDSVIGEGCVIKNCKIHHSVVGLRS
CISEGAIIEDTLLMGADYYETEADKKLLADKGGIPIGIGKNSHIRRAIIDKNARIGDNVKIINVDNVQEAA
RETDGYFIKSGIVTVIKDALLPSGTVI

Fig. 30

MAATMTVEEVRKAQRAEGPATVLAIGTATPANCVYQADYPDYYFKITKSDHLADLKEKFKRMCDKSQIRKR
YMHLTEEILEENPNMCAYMAPSLDARQDIVVVEVPKLGKAAAQKAIKEWGQPRSKITHLVFCTTSGVDMPG
ADYQLTKMLGLRPSVKRLMMYQQGCFAGGTVLRLAKDLAENNRGARVLVVCSEITAVTFRGPHESHLDSLV
GQALFGDGAAAVIIGADPDVSVERPLFQLVSVSQTILPDSEGAIDGHLREVGLTFHLLKDVPGLISKNIER
ALEEAFKPLGIDDWNSVFWVAHPGGPAILDMVEAKVNLNKERMRATRHVLSEYGNMSSACVLFIMDEMRKR
SAEDGHTTTGEGMDWGVLFGFGPGLTVETVVLHSMPIAADATA

Fig. 31

MATTMTVEEVRKAQRAEGPATVLAIGTATPANCVYQADYPDYYFKITKSDHLADLKEKFKRMCDKSQIRKR
YMHLTEEILEENPNMCAYMAPSLDARQDIVVVEVPKLGKAAAQKAIKEWGQPRSKITHLVFCTTSGVDMPG
ADYQLTKMLGLRPSVKRLMMYQQGCFAGGTVLRLAKDLAENNRGARVLVVCSEITAVTFRGPHESHLDSLV
GQALFGDGAAAVIIGADPDVSVEHPLFQLVSASQTILPDSEGAIDGHLREVGLTFHLLKDVPGLISKNIER
ALEEAFKPLGIDDWNSVFWVAHPGGPAILDMVEAKVNLNKERMRATRHVLSEYGNMSSACVLFIMDEMRKR
SAEDGHTTTGEGMDWGVLFGFGPGLTVETVVLHSMPIAAGATA

Fig. 32

RADLEEEGSFDDAVAGCDYAFLVAAPVNLKAENPEKDMVEPAVGGTLNAMRSCVRAGTVKRVVLTSSVASV
SARPLLQGDGHVLDEESWSDVDFLRAKATGHWGYPVSKVLLEKAACAFAQASGISLVTVCPVVVVGKAPAV
QVHTSVPDVLSPLSGDEAKIQILQHIERASGSISLVHVDDLCRAEVFLAEEEAVASGRYICCSLSTTAGVL
ARFLSVKYPQYKVRTDRFSGSPEKPRVCMSSAKLVAEGFQYKYKTLDEIYDDVVEYGRALGILP

Fig. 33

MAAAGDGSRRKTACVTGGNGYIASALVKMLLEKGYAVKTTVRNPDDMEKNSHLKDLQALGPLEVFRADLQE
EGSFDDAVAGCDYAFLVAAPVNLKAENPEKDMVEPAVGGTLNAMRSCVRAGTVKRVVLTSSVASVSARPLL
QGDGHVLDEESWSDVDFLRAKATGHWGYPVSKVLLEKAACAFAQASGISLVTVCPVVVVGKAPAVQVHTSV
PDVLSPLSGDEAKIQILQHIERASGSISLVHVDDLCRAEVFLAEEEAVASGRYICCSLSTTAGVLARFLSV
KYPQYKVRTDRFSGSPEKPRVCMSSAKLVAEGFQYKYKTLDEIYDDVVEYGRALGILP

Fig. 34

FISVTVFYVVGLRQRDLVQAGVQGTLNVMRSCVKAGTVKRVILTSSDSAVCQRPLEGDGHVLDEGSWSDVP
YLRAEQPEAWGYAVSKVLMEEAAGKFADENGLGLVSVLPTFTLGAAPVSQARTSVPVVLSLLSGDEEQLNL
LEAMHLITESVSINHIDDLCRAQVFLAENEASSGRYICSSHDTTVVQLARLLADKYPQYNVKSQRFDGSPE
KPRVCLSSQKLIGEGFVYKYDDLGAILDDLVEYGRTTGILPF

Fig. 35

MASAAGGRRKTACVTGGSGYIASALIKTLLDHGYAVKTTVRNPDDLEKTSHLKDLQAFGPLEIFRGELDVE
GSFDDSVSGCDYVFLVAAPMDMGSLNPERDLVQAGVQGTLNVMRSCVKAGTVKRVILTSSDSAVCQRPLEG
DGHVLDEGSWSDVPYLRAEQPEAWGYAVSKVLMEEAAGKFADENGLGLVSVLPTFTLGAAPVSQARTSVPV
VLSLLSGDEEQLNLLEAMHLITESVSINHIDDLCRAQVFLAENEASSGRYICSSHDTTVVQLARLLADKYP
QYNVKSQRFDGSPEKPRVCLSSQKLIGEGFVYKYDDLGAILDDLVEYGRTTGILPFAAASIWFLFRGSSSG
KKLSKLPLPPGPRGWPVLGNLPQVGAKPHHTMAALSQQFGPLFRLRFGVAEVVVAASAKVASQFLRAHDAN
FSDRPPNSGAEHVAYNYQDLVFAPYGSRWRALRKLCALHLFSAKALDALRAVREAEVALMVKQLKESAPAG
VVVGQEANVCATNALARAAVGRRVFGGSAGEGAREFKDMVVELMQLAGVFNIGDFVPALRWLDPQGVVARM
KRLHRRYDAMMDGFISERDQRHNQAAADGERKDLLSVMLGYMRPDGGGGEEEGISFNHTDIKALLLNLFTA
GTDTTSSTVEWALAELIRHKDVLTQAQRELDDIVGQDRLVTESDLPHLTFLTAVIKETFRLHPSTPLSLPR
VATEDCEVEGYRIPKGTTLLVNVWAIARDPASWGPDALEFRPARFLAGGLHESVDVKGSDYELIPFGAGRR
ICAGLSWGLRMVTLMTATLVHAFDWSLVDGLTPEKLDMEEAYGLTLQRAAPLMVRPIPRLLSSAYTV

Fig. 36

MDHRDVLVLLCSLAALAAASIWFLFRGSSSGKKLSKLPLPPGPRGWPVLGNLPQVGAKPHHTMAALSQQFG
PLFRLRFGVAEVVVAASAKVASQFLRAHDANFSDRPPNSGAEHVAYNYQDLVFAPYGSRWRALRKLCALHL
FSAKALDALRAVREAEVALMVKQLKESAPAGVVVGQEANVCATNALARAAVGRRVFGGSAGEGAREFKDMV
VELMQLAGVFNIGDFVPALRWLDPQGVVARMKRLHRRYDAMMDGFISERDQRHNQAAADGERKDLLSVMLG
YMRPDGGGGEEEGISFNHTDIKALLLNLFTAGTDTTSSTVEWALAELIRHKDVLTQAQRELDDIVGQDRLV
TESDLPHLTFLTAVIKETFRLHPSTPLSLPRVATEDCEVEGYRIPKGTTLLVNVWAIARDPASWGPDALEF
RPARFLAGGLHESVDVKGSDYELIPFGAGRRICAGLSWGLRMVTLMTATLVHAFDWSLVDGLTPEKLDMEE
AYGLTLQRAAPLMVRPIPRLLSSAYTV

Fig. 37

RSELAGMDIPLSLLLSTLAISATICYVFFRAGKGHRAPLPLPPGPRGWPVLGNLPQLGGKTHQTLHEMTKV
YGPVLRLRFGSSVVVVAGSAAVAEQFLRTHDAKFSSRPPNSGGEHMAYNYRDVVFAPYGPRWRAMRKVCAV
NIFSARALDDLRGFREREAALMVRSLADAAKAGVAVAVGKAANVCTTNGLSRAAVGLRVFGSDGARDFKEI
VLEVMEVGGVLNVGDFVPALRWLDPQGVVARLKKLHRRFDDMMNGIIAERRTGTKTAVVEEGKGDLLGLLL
AMVQEDKSLTGSEEDKITDTDVKALILNLFVAGTETTSSIVEWAVAELIRHPDILKQAQEELDAVVGRDRL
VSESDLPRLTFFNAIIKETFRLHPSTPLSLPRMASEECEVAGYHIPRGTELLVNVWGIARDPALWPDPLEY
QPARFLPGGSHENVDLKGGDFGLIP$\boxed{\text{FGAGRRICAG}}$LSWGLRMVTITTATLVHSFDWELPAGQTPDKLNMEE
AFSLLLQRAVPLMVHPVPRLLPSAYEIS

Fig. 38

MRSELAGMDIPLPLLLSTLAISATICYVFFRAGKGHRAPLPLPPGPRGWPVLGNLPQLGGKTHQTLHEMTK
VYGPVLRLRFGSSVVVVAGSAAVAEQFLRTHDAKFSSRPPNSGGEHMAYNYRDVVFAPYGPRWRAMRKVCA
VNIFSARALDDLRGFREREAALMVRSLADAAKAGVAVAVGKAANVCTTNGLSRAAVGLRVFGSDGARDFKE
IVLEVMEVGGVLNVGDFVPALRWLDPQGVVARLKKLHRRFDDMMNGIIAERRTGTKTAVVEEGKGDLLGLL
LAMVQEDKSLTGSEEDKITDTDVKALILNLFVAGTETTSSIVEWAVAELIRHPDILKQAQEELDAVVGRDR
LVSESDLPRLTFFNAIIKETFRLHPSTPLSLPRMASEECEVAGYHIPRGTELLVNVWGIARDPALWPDPLE
YQPARFLPGGSHENVDLKGGDFGLIP$\boxed{\text{FGAGRRICAG}}$LSWGLRMVTITTATLVHSFDWELPAGQTPDKLNME
EAFSLLLQRAVPLMVHPVPRLLPSAYEIS

Fig. 39

DIPLPLLLSTLAISATICYVFFRAGKTHQTLHEMTKVYGPVLRLRFGSSVVVVAGSAAVAEQFLRTHDAKF
SSRPPNSGGEHMAYNYQDIVFAPYGPRWRAMRKVCAVNIFSARALDDLRGFREREAALMVRSLADAAKAGA
AVAVGKAANVCTTNGLSRAAVGLRVFGSDGTRDFKEIVLEVMEVGGVLNVGDFVPALRWLDPQGVVARMKK
LHRRFDDIMNGIIAERRTGAKTAVVEEGKGDLLGLLLAMVQEDKSLTGSEEDKITDTDVKALILNLFVAGT
ETTSSIVEWAVAELIRHPDILKQAQEELDTVVGRDRIVSESDLPRLTFFNAIIKETFRLHPSTPLSLPRMA
SEDCEVAGYHIPRGTELLVNVWGIARDPSLWPDPLEYRPARFLPGGSHENVDLKGGDFGLIP$\boxed{\text{FGAGRRICA}}$
$\boxed{\text{G}}$LSWGLRMVTVTTATLVHSFDWELPAGQTLDKLNMEEAFSLLLQRAMPLMVHPVPRLLPSAYEIS

Fig. 40

MRNELAGMDIPLPLLLSTLAISATICYVFFRAGKTHQTLHEMTKVYGPVLRLRFGSSVVVVAGSAAVAEQF
LRTHDAKFSSRPPNSGGEHMAYNYQDIVFAPYGPRWRAMRKVCAVNIFSARALDDLRGFREREAALMVRSL
ADAAKAGAAVAVGKAANVCTTNGLSRAAVGLRVFGSDGTRDFKEIVLEVMEVGGVLNVGDFVPALRWLDPQ
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Fig. 41

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SEQUENCE LISTING

<110> Demmer, Jeroen
Shenk, Michael Andrew
Glenn, Matthew
Norriss, Michael Geoffrey
Saulsbury, Keith Martin
Hall, Claire
Forster, Richard L. S.

<120> Compositions isolated from forage grasses and methods for their use.

<130> 11000.1069PCT

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<170> FastSEQ for Windows Version 4.0

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<211> 1697
<212> DNA
<213> Festuca arundinacea

<400> 2
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<211> 2174
<212> DNA
<213> Lolium perenne

<400> 3

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<211> 2478
<212> DNA
<213> Lolium perenne

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<213> Lolium perenne

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<212> DNA
<213> Festuca arundinacea

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<211> 2250
<212> DNA

<213> Festuca arundinacea

<400> 7
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<211> 973
<212> DNA
<213> Lolium perenne

<400> 8
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<211> 2019

<212> DNA
<213> Lolium perenne

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<210> 10
<211> 2457
<212> DNA
<213> Lolium perenne

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<213> Lolium perenne

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<213> Lolium perenne

<400> 12

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<213> Festuca arundinacea

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<213> Lolium perenne

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<213> Lolium perenne

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<213> Festuca arundinacea

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<212> DNA
<213> Festuca arundinacea

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<213> Festuca arundinacea

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<213> Festuca arundinacea

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<212> DNA
<213> Lolium perenne

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<210> 29
<211> 2063
<212> DNA
<213> Festuca arundinacea

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<212> DNA
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<212> DNA
<213> Festuca arundinacea

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<211> 1494
<212> DNA
<213> Festuca arundinacea

<400> 32
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ggagggcaaa gctccaatta taccatgcac tactatcgat gggttatctc accgtttgaa 1680
ctaaagtagt ttacaatgca tattgttccg agaagttcaa taagaaagaa taacatgaaa 1740
aaaaaaa 1747

<210> 41
<211> 1763
<212> DNA
<213> Festuca arundinacea

<400> 41
gaacagttgc cgtgcatgcg tagcgagctg gctggcatgg acatcccact cccactgctg 60
ctctccactc tggccatctc tgcgaccata tgctatgtct tcttccgagc cggcaagggg 120
caccgtgcgc cgctgccgct gccgcctggc ccgaggggct ggccagtgct ggggaacctc 180
ccgcagctgg gcggcaagac acaccagacc ctgcatgaga tgaccaaggt gtacgggccc 240
gtgctccggc tccggttcgg cagctccgtc gtggtggtcg ccgggtcagc cgccgtggcc 300
gagcagttcc tccgcaccca cgacgccaag ttcagcagcc ggccgcccaa ctccggcggc 360
gaacacatgg cgtacaacta cagggacgtg gttttcgcgc cctacggccc ccggtggcgc 420
gcgatgcgca aggtgtgcgc cgtcaacatc ttctcggccc gcgcgctcga cgatctccgc 480
ggtttcaggg agcgggaggc cgcgctcatg gtgcggtccc tcgcggatgc tgccaaagcc 540

```
ggggtggcgg tggcggtcgg caaggcggcg aacgtgtgca cgaccaacgg cctgtctcgg   600
gcagcggtgg ggctccgggt gttcggaagc gatggcgcca gagacttcaa ggagatcgtg   660
ctggaggtga tggaggtggg cggggttctt aacgtcgggg actttgtgcc ggcgctccgg   720
tggctcgacc cgcagggtgt cgtcgcgagg ttgaagaagc tgcaccgccg gttcgacgac   780
atgatgaatg ggataatcgc cgagaggagg accggaacca agacggccgt ggtggaggaa   840
ggtaagggag acctgctggg cttgctgctt gcgatggtgc aggaagacaa gtcgctcacc   900
ggcagcgagg aggacaagat caccgacact gacgtcaagg cgcttatact gaacttgttt   960
gtggcgggaa cagagacaac gtcgagtata gtggagtggg cagtagcgga gctgatcagg  1020
caccctgaca tcctgaagca ggcccaggag gagctagatg ccgtcgtggg ccgtgacagg  1080
cttgtctcgg agtctgacct gccacgactc acgtttttca atgccatcat caaggagacg  1140
ttccggctgc atccgtcgac gccgctctcg cttccccgga tggcctccga ggagtgcgag  1200
gtcgccggct accacatccc aaggggcact gagctactgg tcaatgtgtg ggcatcgcc   1260
cgcgatccgg ccctatggcc cgacccgctg gagtaccagc ctgcccggtt cctcccagga  1320
gggtcgcatg agaatgtcga cctcaaggga ggtgactttg ggctgatacc gtttgggcg   1380
ggccggagga tatgtgcggg cctaagctgg ggcttgcgga tggttaccat tacaaccgct  1440
accctggtgc actcgttcga ctgggagctg ccggcgggcc agacgccgga taagttgaac  1500
atggaggagg cctttagtct gctgctgcag cgagccgtgc cattgatggt ccacccagtg  1560
cccaggttgc ttccatccgc atacgaaatt tcgtagaaaa tcgctgcgcc agtgattgtc  1620
ctgattgatg atgtatggag ggcaaagctc caattatacc atgcactact atcgatgggt  1680
tatctcaccg tttgaactaa agtagtttac aatgcatatt gttccgagaa gttcaataag  1740
aaagaataac atgaaaaaaa aaa                                          1763
```

<210> 42
<211> 1673
<212> DNA
<213> Festuca arundinacea

<400> 42

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gggacatccc actcccactg ctgctctcca ctctggccat ctctgcgacc atatgctatg    60
tcttcttccg agccggcaag acacaccaga ccctgcatga gatgaccaag gtgtacgggc   120
ccgtgctccg gctccggttc ggcagctccg tggtggtagt ggccggatca gccgccgtgg   180
ccgagcagtt cctgcgcacc cacgacgcca agttcagcag ccggccgccc aactctggcg   240
gcgagcacat ggcttacaac taccaggaca tcgtgttcgc gccctacggg ccccggtggc   300
gcgccatgcg caaggtgtgc gccgtcaaca tcttctcggc ccgcgcgctc gacgatctcc   360
gcgggttcag ggagcgggag gccgcactca tggtgcggtc cctcgcagac gctgccaaag   420
ccggggcggc ggtggcggtc ggcaaggcgg caaacgtgtg cacgaccaac ggcctgtctc   480
gggcggcggt ggggctccgg gtgttcggaa gcgatggcac cagagacttc aaggagatcg   540
tgctggaggt gatggaggtg ggtggggttc ttaatgtcgg ggattttgtg ccggcgctcc   600
ggtggctcga cccacagggg gtcgtcgcga ggatgaagaa gctgcaccgc cggttcgacg   660
acataatgaa cgggataata gccgagagga ggaccggagc caagacggcc gtcgtggagg   720
aaggtaaggg agacctgctg ggcttgctac ttgcgatggt gcaggaagac aagtcgctca   780
ccggcagcga ggaggacaaa atcaccgaca ctgacgtcaa ggcgcttata ctgaacttgt   840
ttgtggcggg aacagagaca acgtcgagca tagtggagtg ggcagtagcg gagctgatca   900
ggcaccctga catcctgaag caggcccagg aggagctaga taccgtcgtg ggccgtgaca   960
ggatcgtctc ggagtcggac ctgccacgac tcaccttttt taatgccatc atcaaggaga  1020
cgttccggct gcatccgtcg acgccgctct cgcttccccg gatggcctcc gaggactgtg  1080
aggtcgctgg ctaccacatc ccaaggggca ccgagctact ggtcaatgtg tggggcatcg  1140
cccgtgaccc atccctatgg cctgacccgc tggagtaccg gcccgcccgg ttcctcccag  1200
gagggtcgca tgagaatgtc gacctcaagg gaggtgactt tgggctgata ccgtttgggg  1260
cgggccggag gatatgtgcg ggcctaagct ggggcttgcg gatggtcacc gttacaaccg  1320
ctaccctggt gcactcgttc gactgggagc tgccggcggg ccagacgctg gataagttga  1380
acatggagga ggcctttagc ctgctgctgc agcgagccat gccattgatg gtccacccgg  1440
tgcccaggtt gcttccatcg gcatacgaaa tttcgtagaa aattgctgcg ccagtgcttg  1500
tcatgattga tgatgtatgg agggcaagct ccaattatac catgcactac tatcgatggg  1560
ttgtctcccc gtttgaacta aagtagttta caatgcatat tgttccgaga agttcaataa  1620
gaaagaataa catggaaaaa tacaatctgt tggacggcca aaaaaaaaaa aaa         1673
```

<210> 43
<211> 1714
<212> DNA
<213> Festuca arundinacea

<400> 43

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gaaagaacag ttgccgtgca tgcgtaacga gctggctggc atggacatcc cactcccact    60
gctgctctcc actctggcca tctctgcgac catatgctat gtcttcttcc gagccggcaa   120
gacacaccag accctgcatg agatgaccaa ggtgtacggg cccgtgctcc ggctccggtt   180
cggcagctcc gtggtggtag tggccggatc agccgccgtg gccgagcagt tcctgcgcac   240
ccacgacgcc aagttcagca gccggccgcc caactctggc ggcgagcaca tggcttacaa   300
```

```
ctaccaggac atcgtgttcg cgccctacgg gccccggtgg cgcgccatgc gcaaggtgtg    360
cgccgtcaac atcttctcgg cccgcgcgct cgacgatctc cgcgggttca gggagcggga    420
ggccgcactc atggtgcggt ccctcgcaga cgctgccaaa gccggggcgg cggtggcggt    480
cggcaaggcg gcaaacgtgt gcacgaccaa cggcctgtct cgggcggcgg tggggctccg    540
ggtgttcgga agcgatggca ccagagactt caaggagatc gtgctggagg tgatggaggt    600
gggtggggtt cttaatgtcg gggattttgt gccggcgctc cggtggctcg acccacaggg    660
ggtcgtcgcg aggatgaaga agctgcaccg ccggttcgac gacataatga acgggataat    720
agccgagagg aggaccggag ccaagacggc cgtcgtggag gaaggtaagg gagacctgct    780
gggcttgcta cttgcgatgg tgcaggaaga caagtcgctc accggcagcg aggaggacaa    840
aatcaccgac actgacgtca aggcgcttat actgaacttg tttgtggcgg gaacagagac    900
aacgtcgagc atagtggagt gggcagtagc ggagctgatc aggcaccctg acatcctgaa    960
gcaggcccag gaggagctag ataccgtcgt gggccgtgac aggatcgtct cggagtcgga   1020
cctgccacga ctcacctttt ttaatgccat catcaaggag acgttccggc tgcatccgtc   1080
gacgccgctc tcgcttcccc ggatggcctc cgaggactgt gaggtcgctg gctaccacat   1140
cccaaggggc accgagctac tggtcaatgt gtggggcatc gcccgtgacc catccctatg   1200
gcctgacccg ctggagtacc ggcccgcccg gttcctccca ggagggtcgc atgagaatgt   1260
cgacctcaag ggaggtgact ttgggctgat accgtttggg gcgggccgga ggatatgtgc   1320
gggcctaagc tggggcttgc ggatggtcac cgttacaacc gctaccctgg tgcactcgtt   1380
cgactgggag ctgccggcgg gccagacgct ggataagttg aacatggagg aggcctttag   1440
cctgctgctg cagcgagcca tgccattgat ggtccacccg gtgcccaggt tgcttccatc   1500
ggcatacgaa atttcgtaga aaattgctgc gccagtgctt gtcatgattg atgatgtatg   1560
gagggcaagc tccaattata ccatgcacta ctatcgatgg gttgtctccc cgtttgaact   1620
aaagtagttt acaatgcata ttgttccgag aagttcaata agaaagaata acatggaaaa   1680
atacaatctg ttggacggcc aaaaaaaaaa aaaa                               1714
```

<210> 44
<211> 1449
<212> DNA
<213> Lolium perenne

<400> 44

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gacaaacacc ttaactagat cagctcgatc agcttccagc ttcctctcct agctagctcg     60
ctcgctctta tcgccggtga actgtccccc ggccccggta ctaagctgcg cagggcatgg    120
caatggcgga ctgcatgcag gagtggccgg agcccgtggt gcgcgtgcag gcggtggccg    180
agagcggtct ggccgccatc cccgactgct acgtcaagcc gccgcgcgac cgcccagcgg    240
cgcagcacct ggctaccgcc gcttctgcag atggcgacgt cctccatgag cctctggaca    300
ccagcattcc ggtgatcgac cttggcgagc tcgtcgcggc gacagccgac gagggccgca    360
tgcgccagat catggaggcc gtggcggcgg cgtgccggga gtgggggttc ttccaggtgg    420
tgaaccacgg ggtggcgccg gagctgatgc acgcggcgcg ggaggcgtgg cgcggattct    480
tccggctgcc gatcacggcg aagcagcagt acgccaacct gccgcggacg tacgaggggt    540
acggcagccg agtcggcgtc cagaagggcg gcccccctcga ctggggcgac tactatttcc    600
tccacctcgc gccggacgcc ggcaagagcc cggacaagta ctggcccacc aatcccgcca    660
tctgcaagga tgtgtcggag gagtacggtc gtgaggtgat ccggttgtgc gagctgctga    720
tgaaggtgat gtcggcgagc ctgggcctag aggcgacgag gttccaggag gcgttcggcg    780
gatcagagtg cggcgtgtgc cttcgcgcca actactaccc gcggtgcccg cagccggatc    840
tgacgctggg cctgtcggcg cactctgacc cgggcgtcct caccgtgctc ctcgctgacg    900
agcacgtccg cggcctccag gtccgccgcg ccgatggcga gtgggtcacc gtgcagcccg    960
cacggcacga cgccttcatc gtcaacgtcg gcgaccagat ccagatactg agcaactcca   1020
tgtacaagag cgtggagcac cgggtgatgg tgaacgccaa ggaggagcgc atctccctgg   1080
cgctcttcta caacccgcga ggcgacgtcc cgatcgcgcc ggcgccggag acggtgacgc   1140
cggagcggcc ggcgctctac ccgtccatga ccttcgacga gtacagggcc tacatcagga   1200
agtacggccc caggggcaag gcgcaggtcg agggtgccaa gcagggacaa ggtagctagt   1260
tagctggatc cttggagcta gtatctgatc catgggaata attaagccgt ccaggttgta   1320
ccggccaatc tatggattcc tgcatgcatg tacgtgtggc taatgtagca caagctcgcc   1380
cttgtacccg aactgcatat atgctaattg tattggcatc tcgcttagcc gtgccgtcca   1440
aaaaaaaaa                                                           1449
```

<210> 45
<211> 473
<212> PRT
<213> Lolium perenne

<400> 45

```
Met Ala Ala Ala Ala Val Ala Pro Asp Ala Lys Ile Glu Lys Phe Arg
1               5                   10                  15
Asp Ala Val Ala Lys Leu Gly Glu Ile Ser Glu Asn Glu Lys Ala Gly
            20                  25                  30
Cys Ile Ser Leu Val Ser Arg Tyr Leu Ser Gly Glu Ala Glu Gln Ile
```

```
                35                      40                      45
Glu Trp Ser Lys Ile Gln Thr Pro Thr Asp Glu Val Val Val Pro Tyr
    50                  55                      60
Asp Thr Leu Ala Pro Ala Pro Glu Asp Leu Asp Ala Met Lys Ala Leu
65                  70                      75                  80
Leu Asp Lys Leu Val Val Leu Lys Leu Asn Gly Gly Leu Gly Thr Thr
                85                      90                  95
Met Gly Cys Thr Gly Pro Lys Ser Val Ile Glu Val Arg Asn Gly Phe
            100                     105                 110
Thr Phe Leu Asp Leu Ile Val Ile Gln Ile Glu Ser Leu Asn Lys Lys
        115                     120                 125
Tyr Gly Cys Asp Val Pro Leu Leu Leu Met Asn Ser Phe Asn Thr His
    130                 135                     140
Asp Asp Thr Gln Lys Ile Val Glu Lys Tyr Ser Asn Ser Asn Ile Asn
145                 150                     155                 160
Ile His Thr Phe Asn Gln Ser Gln Tyr Pro Arg Ile Val Thr Glu Asp
                165                     170                 175
Phe Leu Pro Leu Pro Ser Lys Gly Gln Ser Gly Lys Asp Gly Trp Tyr
            180                     185                 190
Pro Pro Gly His Gly Asp Val Phe Pro Ser Leu Asn Asn Ser Gly Lys
        195                     200                 205
Leu Asp Thr Leu Leu Ser Gln Gly Lys Glu Tyr Val Phe Val Ala Asn
    210                 215                     220
Ser Asp Asn Leu Gly Ala Ile Val Asp Ile Lys Ile Leu Asn His Leu
225                 230                     235                 240
Ile Asn Asn Lys Asn Glu Tyr Cys Met Glu Val Thr Pro Lys Thr Leu
                245                     250                 255
Ala Asp Val Lys Gly Gly Thr Leu Ile Ser Tyr Glu Gly Arg Val Gln
            260                     265                 270
Leu Leu Glu Ile Ala Gln Val Pro Asp Glu His Val Asn Glu Phe Lys
        275                     280                 285
Ser Ile Glu Lys Phe Lys Ile Phe Asn Thr Asn Asn Leu Trp Val Asn
    290                 295                     300
Leu Lys Ala Ile Lys Arg Leu Val Glu Ala Asp Ala Leu Lys Met Glu
305                 310                     315                 320
Ile Ile Pro Asn Pro Lys Glu Val Asp Gly Val Lys Val Leu Gln Leu
                325                     330                 335
Glu Thr Ala Ala Gly Ala Ala Ile Arg Phe Phe Asp Asn Ala Ile Gly
            340                     345                 350
Ile Asn Gly Pro Arg Ser Arg Phe Leu Pro Val Lys Ala Thr Ser Asp
        355                     360                 365
Leu Leu Leu Val Gln Ser Asp Leu Tyr Thr Leu Val Asp Gly Tyr Val
    370                 375                     380
Ile Arg Asn Pro Ala Arg Val Lys Pro Ser Asn Pro Ser Ile Glu Leu
385                 390                     395                 400
Gly Pro Glu Phe Lys Lys Val Ala Ser Phe Leu Ala Arg Phe Lys Ser
                405                     410                 415
Ile Pro Ser Ile Val Glu Leu Asp Ser Leu Lys Val Ser Gly Asp Val
            420                     425                 430
Ser Phe Gly Ser Gly Ile Val Leu Lys Gly Asn Val Thr Ile Ala Ala
        435                     440                 445
Lys Ser Gly Val Lys Leu Glu Ile Pro Asp Gly Ala Val Leu Glu Asn
    450                 455                     460
Lys Asp Ile Asn Gly Pro Glu Asp Leu
465                 470
```

<210> 46
<211> 471
<212> PRT
<213> Festuca arundinacea

```
<400> 46
Met Ala Ala Val Ala Ala Asp Ala Lys Ile Glu Lys Phe Arg Asp Ala
 1              5                   10                  15
Val Ala Lys Leu Asp Glu Ile Ser Glu Asn Glu Lys Ala Gly Cys Ile
            20                  25                  30
Ser Leu Val Ser Arg Tyr Leu Ser Gly Glu Ala Glu Gln Ile Glu Trp
        35                  40                  45
```

Ser Lys Ile Gln Thr Pro Thr Asp Glu Val Val Val Pro Tyr Asp Thr
50 55 60
Leu Ala Pro Ala Pro Gln Asp Leu Asp Ala Met Lys Ala Leu Leu Asp
65 70 75 80
Lys Leu Val Val Leu Lys Leu Asn Gly Gly Leu Gly Thr Thr Met Gly
85 90 95
Cys Thr Gly Pro Lys Ser Val Ile Glu Val Arg Asn Gly Phe Thr Phe
100 105 110
Leu Asp Leu Ile Val Ile Gln Ile Glu Ser Leu Asn Lys Lys Tyr Gly
115 120 125
Cys Asp Val Pro Leu Leu Leu Met Asn Ser Phe Asn Thr His Asp Asp
130 135 140
Thr Gln Lys Ile Val Glu Lys Tyr Ser Asn Ser Asn Ile Asn Ile His
145 150 155 160
Thr Phe Asn Gln Ser Gln Tyr Pro Arg Ile Val Thr Glu Asp Phe Leu
165 170 175
Pro Leu Pro Ser Lys Gly Lys Ser Gly Lys Asp Gly Trp Tyr Pro Pro
180 185 190
Gly His Gly Asp Val Phe Pro Ser Leu Asn Asn Ser Gly Lys Leu Asp
195 200 205
Thr Leu Leu Ser Gln Gly Lys Glu Tyr Val Phe Val Ala Asn Ser Asp
210 215 220
Asn Leu Gly Ala Ile Val Asp Ile Lys Ile Leu Asn His Leu Ile Asn
225 230 235 240
Asn Gln Asn Glu Tyr Cys Met Glu Val Thr Pro Lys Thr Leu Ala Asp
245 250 255
Val Lys Gly Gly Thr Leu Ile Ser Tyr Glu Gly Arg Val Gln Leu Leu
260 265 270
Glu Ile Ala Gln Val Pro Asp Glu His Val Asn Glu Phe Lys Ser Ile
275 280 285
Glu Lys Phe Lys Ile Phe Asn Thr Asn Asn Leu Trp Val Asn Leu Lys
290 295 300
Ala Ile Lys Arg Leu Val Glu Ala Asp Ala Leu Lys Met Glu Ile Ile
305 310 315 320
Pro Asn Pro Lys Glu Val Asp Gly Val Lys Val Leu Gln Leu Glu Thr
325 330 335
Ala Ala Gly Ala Ala Ile Arg Phe Phe Glu Lys Ala Ile Gly Ile Asn
340 345 350
Gly Pro Arg Ser Arg Phe Leu Pro Val Lys Ala Thr Ser Asp Leu Leu
355 360 365
Leu Val Gln Ser Asp Leu Tyr Thr Leu Val Asp Gly Tyr Val Ile Arg
370 375 380
Asn Pro Ala Arg Val Lys Pro Ser Asn Pro Ser Ile Glu Leu Gly Pro
385 390 395 400
Glu Phe Lys Lys Val Ala Ser Phe Leu Ala Arg Phe Lys Ser Ile Pro
405 410 415
Ser Ile Val Glu Leu Asp Ser Leu Lys Val Ser Gly Asp Val Thr Phe
420 425 430
Gly Ser Gly Val Val Leu Lys Gly Asn Val Thr Ile Ala Ala Lys Ser
435 440 445
Gly Val Lys Leu Glu Ile Pro Asp Gly Ala Val Leu Glu Asn Lys Asp
450 455 460
Ile Asn Gly Pro Glu Asp Leu
465 470

<210> 47
<211> 535
<212> PRT
<213> Lolium perenne

<400> 47
Cys Leu Arg Arg Arg Thr Tyr Ser Asn Ser Gly Asp Thr His Ala Asp
1 5 10 15
Pro Asn Gly Pro Val Tyr Tyr Gly Gly Trp Tyr His Leu Phe Tyr Gln
20 25 30
His Asn Pro Tyr Gly Asp Ser Trp Gly Asn Val Ser Trp Gly His Ala
35 40 45
Val Ser Lys Asp Leu Val Asn Trp Arg His Leu Pro Val Ala Leu Val

50 55 60
Pro Asp Gln Trp Tyr Asp Ile Asn Gly Val Leu Thr Gly Ser Ile Thr
65 70 75 80
Val Leu Pro Asp Gly Arg Val Ile Leu Leu Tyr Thr Gly Asn Thr Asp
85 90 95
Thr Phe Ser Gln Val Gln Cys Leu Ala Val Pro Ala Asp Pro Ser Asp
100 105 110
Pro Leu Leu Arg Ser Trp Ile Lys His Pro Ala Asn Pro Ile Leu Phe
115 120 125
Pro Pro Pro Gly Ile Gly Leu Lys Asp Phe Arg Asp Pro Leu Thr Ala
130 135 140
Trp Phe Glu His Ser Asp Asn Thr Trp Arg Thr Ile Ile Gly Ser Lys
145 150 155 160
Asp Asp Asp Gly His Ala Gly Ile Val Leu Ser Tyr Lys Thr Thr Asp
165 170 175
Phe Val Asn Tyr Glu Leu Met Pro Gly Asn Met His Arg Gly Pro Asp
180 185 190
Gly Thr Gly Met Tyr Glu Cys Leu Asp Ile Tyr Pro Val Gly Gly Asn
195 200 205
Ser Ser Glu Met Leu Gly Gly Asp Ser Ser Pro Glu Val Leu Phe Val
210 215 220
Leu Lys Glu Ser Ala Asn Asp Glu Trp His Asp Tyr Tyr Ala Leu Gly
225 230 235 240
Trp Phe Asp Ala Thr Ala Asn Thr Trp Thr Pro Gln Asp Pro Glu Ala
245 250 255
Asp Leu Gly Ile Gly Leu Arg Tyr Asp Trp Gly Lys Tyr Tyr Ala Ser
260 265 270
Lys Ser Phe Tyr Asp Pro Ile Lys Asn Arg Arg Val Val Trp Ala Phe
275 280 285
Val Gly Glu Thr Asp Ser Glu Gln Ala Asp Lys Ala Lys Gly Trp Ala
290 295 300
Ser Leu Met Ser Ile Pro Arg Met Val Glu Leu Asp Lys Lys Thr Arg
305 310 315 320
Thr Asn Leu Ile Gln Trp Pro Val Glu Glu Ile Glu Thr Leu Arg Arg
325 330 335
Asn Val Thr Asp Leu Gly Gly Ile Thr Val Glu Ala Gly Ser Val Ile
340 345 350
His Leu Pro Leu Gln Gln Gly Gly Gln Leu Asp Ile Glu Ala Ser Phe
355 360 365
Arg Leu Asn Ser Ser Asp Ile Asp Ala Leu Asn Glu Ala Asp Val Gly
370 375 380
Phe Asn Cys Ser Ser Ser Ala Gly Ala Ala Val Arg Gly Ala Leu Gly
385 390 395 400
Pro Phe Gly Leu Leu Val Phe Ala Asp Gly Arg His Glu Gln Thr Ala
405 410 415
Ala Tyr Phe Tyr Val Ser Lys Gly Leu Asp Gly Ser Leu Leu Thr His
420 425 430
Tyr Cys His Asp Glu Ser Arg Ser Thr Arg Ala Lys Asp Val Val Ser
435 440 445
Arg Val Val Gly Gly Thr Val Pro Val Leu Asp Gly Glu Thr Phe Ser
450 455 460
Val Arg Val Leu Val Asp His Ser Ile Val Gln Ser Phe Val Met Gly
465 470 475 480
Gly Arg Thr Thr Val Thr Ser Arg Ala Tyr Pro Thr Glu Ala Ile Tyr
485 490 495
Ala Ala Ala Gly Val Tyr Leu Phe Asn Asn Ala Thr Ser Ala Thr Ile
500 505 510
Thr Ala Glu Gly Leu Val Val Tyr Glu Met Ala Ser Ala Glu Ser Gln
515 520 525
Ala Phe Leu Ala Asp Asp Met
530 535

<210> 48
<211> 637
<212> PRT
<213> Lolium perenne

<400> 48

Met Glu Ser Ser Ala Val Val Val Pro Gly Thr Thr Ala Pro Leu Leu
1 5 10 15
Pro Tyr Asp Ser Arg Glu Asn Gln Ser Ser Gly Gly Gly Val Trp Trp
20 25 30
Arg Ala Cys Ala Ala Ser Ala Val Val Leu Leu Val Val Val Gly Phe
35 40 45
Phe Ala Gly Gly Arg Val Asp Leu Gly Gln Ala Gly Glu Val Ser Ala
50 55 60
Thr Ser Ser Val Pro Ala Ala Met Met Glu Ile Pro Arg Ser Arg Gly
65 70 75 80
Lys Asn Phe Gly Val Ser Glu Lys Ala Asp Gly Gly Phe Pro Trp Ser
85 90 95
Asn Ala Met Leu Gln Trp Gln His Thr Gly Phe His Phe Gln Pro Leu
100 105 110
Lys His Tyr Met Asn Asp Pro Asn Gly Pro Val Tyr Tyr Gly Gly Trp
115 120 125
Tyr His Leu Phe Tyr Gln His Asn Pro Tyr Gly Asp Ser Trp Gly Asn
130 135 140
Val Ser Trp Gly His Ala Val Ser Lys Asp Leu Val Asn Trp Arg His
145 150 155 160
Leu Pro Val Ala Leu Val Pro Asp Gln Trp Tyr Asp Ile Asn Gly Val
165 170 175
Leu Thr Gly Ser Ile Thr Val Leu Pro Asp Gly Arg Val Ile Leu Leu
180 185 190
Tyr Thr Gly Asn Thr Asp Thr Phe Ser Gln Val Gln Cys Leu Ala Val
195 200 205
Pro Ala Asp Pro Ser Asp Pro Leu Leu Arg Ser Trp Ile Lys His Pro
210 215 220
Ala Asn Pro Ile Leu Phe Pro Pro Pro Gly Ile Gly Leu Lys Asp Phe
225 230 235 240
Arg Asp Pro Leu Thr Ala Trp Phe Glu His Ser Asp Asn Thr Trp Arg
245 250 255
Thr Ile Ile Gly Ser Lys Asp Asp Asp Gly His Ala Gly Ile Val Leu
260 265 270
Ser Tyr Lys Thr Thr Asp Phe Val Asn Tyr Glu Leu Met Pro Gly Asn
275 280 285
Met His Arg Gly Pro Asp Gly Thr Gly Met Tyr Glu Cys Leu Asp Ile
290 295 300
Tyr Pro Val Gly Gly Asn Ser Ser Glu Met Leu Gly Gly Asp Ser Ser
305 310 315 320
Pro Glu Val Leu Phe Val Leu Lys Glu Ser Ala Asn Asp Glu Trp His
325 330 335
Asp Tyr Tyr Ala Leu Gly Trp Phe Asp Ala Thr Ala Asn Thr Trp Thr
340 345 350
Pro Gln Asp Pro Glu Ala Asp Leu Gly Ile Gly Leu Arg Tyr Asp Trp
355 360 365
Gly Lys Tyr Tyr Ala Ser Lys Ser Phe Tyr Asp Pro Ile Lys Asn Arg
370 375 380
Arg Val Val Trp Ala Phe Val Gly Glu Thr Asp Ser Glu Gln Ala Asp
385 390 395 400
Lys Ala Lys Gly Trp Ala Ser Leu Met Ser Ile Pro Arg Met Val Glu
405 410 415
Leu Asp Lys Lys Thr Arg Thr Asn Leu Ile Gln Trp Pro Val Glu Glu
420 425 430
Ile Glu Thr Leu Arg Arg Asn Val Thr Asp Leu Gly Gly Ile Thr Val
435 440 445
Glu Ala Gly Ser Val Ile His Leu Pro Leu Gln Gln Gly Gly Gln Leu
450 455 460
Asp Ile Glu Ala Ser Phe Arg Leu Asn Ser Ser Asp Ile Asp Ala Leu
465 470 475 480
Asn Glu Ala Asp Val Gly Phe Asn Cys Ser Ser Ser Ala Gly Ala Ala
485 490 495
Val Arg Gly Ala Leu Gly Pro Phe Gly Leu Leu Val Phe Ala Asp Gly
500 505 510
Arg His Glu Gln Thr Ala Ala Tyr Phe Tyr Val Ser Lys Gly Leu Asp
515 520 525
Gly Ser Leu Leu Thr His Tyr Cys His Asp Glu Ser Arg Ser Thr Arg
530 535 540

Ala Lys Asp Val Val Ser Arg Val Val Gly Gly Thr Val Pro Val Leu
545 550 555 560
Asp Gly Glu Thr Phe Ser Val Arg Val Leu Val Asp His Ser Ile Val
565 570 575
Gln Ser Phe Val Met Gly Gly Arg Thr Thr Val Thr Ser Arg Ala Tyr
580 585 590
Pro Thr Glu Ala Ile Tyr Ala Ala Ala Gly Val Tyr Leu Phe Asn Asn
595 600 605
Ala Thr Ser Ala Thr Ile Thr Ala Glu Gly Leu Val Val Tyr Glu Met
610 615 620
Ala Ser Ala Glu Ser Gln Ala Phe Leu Ala Asp Asp Met
625 630 635

<210> 49
<211> 603
<212> PRT
<213> Lolium perenne

<400> 49
Met Gly Ile Ala Glu Val Ala Leu His Thr Met Pro Gly Ala Phe Ala
1 5 10 15
Ser His Ser Pro Ala Ser Ser Leu Pro Leu Arg Thr Asp Thr Arg Ser
20 25 30
Leu Arg Lys Arg Gly Thr Asn Ser Phe Tyr Arg Thr Leu Gly Gly Pro
35 40 45
Pro Lys Phe Pro Glu Leu Arg Pro Val Glu Cys Gln Cys Gln Arg Ile
50 55 60
Asp Asp Leu Ala Gly Val Ile Glu Ala Gly Asn Gly Thr Trp Ala Thr
65 70 75 80
Asp Met Val Asn Lys Ala Ser Gln Val Leu Gly Asp Val Ala Val Pro
85 90 95
Gly Gln Ala Leu Gly Gly Asn Ala Ser Leu Ser Gly Asp Pro Glu Lys
100 105 110
Val Leu Pro Arg Arg Arg Asn Leu Ser Ser Val Glu Asp Glu Ala Trp
115 120 125
Asp Leu Leu Arg Glu Ser Val Val Asn Tyr Cys Gly Ser Pro Val Gly
130 135 140
Thr Ile Ala Ala Asn Asp Pro Asn Asp Ser Asn Pro Ala Asn Tyr Asp
145 150 155 160
Gln Val Phe Ile Arg Asp Phe Ile Pro Ser Gly Ile Ala Phe Leu Leu
165 170 175
Lys Gly Glu Tyr Glu Ile Val Arg Asn Phe Ile Leu His Thr Leu Gln
180 185 190
Leu Gln Ser Trp Glu Lys Thr Met Asp Cys His Ser Pro Gly Gln Gly
195 200 205
Leu Met Pro Ala Ser Phe Lys Val Arg Thr Ile Pro Leu Asp Gly Asp
210 215 220
Glu Asn Ala Thr Glu Glu Val Leu Asp Pro Asp Phe Gly Glu Ala Ala
225 230 235 240
Ile Gly Arg Val Ala Pro Val Asp Ser Gly Leu Trp Trp Ile Ile Leu
245 250 255
Leu Arg Ala Tyr Gly Lys Cys Ser Gly Asp Leu Ser Val Gln Glu Arg
260 265 270
Ile Asp Val Gln Thr Gly Ile Lys Met Ile Leu Lys Leu Cys Leu Ala
275 280 285
Asp Gly Phe Asp Met Phe Pro Thr Leu Leu Val Thr Asp Gly Ser Cys
290 295 300
Met Ile Asp Arg Arg Met Gly Ile His Gly His Pro Leu Glu Ile Gln
305 310 315 320
Ala Leu Phe Tyr Ser Ala Leu Leu Ser Ala Arg Glu Met Leu Thr Pro
325 330 335
Glu Asp Gly Ser Ala Asp Leu Ile Arg Ala Leu Asn Asn Arg Leu Val
340 345 350
Ala Leu Ser Phe His Ile Arg Glu Tyr Tyr Trp Val Asp Met Gln Lys
355 360 365
Leu Asn Glu Ile Tyr Arg Tyr Lys Thr Glu Glu Tyr Ser Tyr Asp Ala
370 375 380
Val Asn Lys Phe Asn Ile Tyr Pro Asp Gln Val Ser Pro Trp Leu Val

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385                 390                 395                 400
Glu Trp Ile Pro Pro Lys Gly Gly Tyr Phe Ile Gly Asn Leu Gln Pro
                405                 410                 415
Ala His Met Asp Phe Arg Phe Phe Ser Leu Gly Asn Leu Trp Ser Ile
            420                 425                 430
Val Ser Ser Leu Ala Thr Thr Gln Gln Ser His Ala Ile Leu Asp Leu
        435                 440                 445
Ile Glu Ser Lys Trp Ser Asp Leu Val Ala Glu Met Pro Leu Lys Ile
    450                 455                 460
Cys Tyr Pro Ala Leu Glu Asn Leu Glu Trp Lys Ile Ile Thr Gly Ser
465                 470                 475                 480
Asp Pro Lys Asn Thr Pro Trp Ser Tyr His Asn Gly Gly Ser Trp Pro
                485                 490                 495
Thr Leu Leu Trp Gln Leu Thr Val Ala Ser Leu Lys Met Asn Arg Pro
            500                 505                 510
Glu Ile Ala Ala Lys Ala Val Glu Ile Ala Glu Arg Arg Ile Ala Thr
        515                 520                 525
Asp Lys Trp Pro Glu Tyr Tyr Asp Thr Lys Arg Ala Arg Phe Ile Gly
    530                 535                 540
Lys Gln Ser Arg Leu Tyr Gln Thr Trp Ser Ile Ala Gly Tyr Leu Val
545                 550                 555                 560
Ala Lys Gln Leu Leu Asp Lys Pro Asp Ala Ala Arg Ile Leu Trp Asn
                565                 570                 575
Asp Glu Asp Thr Glu Ile Leu Asn Ala Phe Ser Thr Asn Arg Lys Arg
            580                 585                 590
Gly Lys Lys Val Leu Lys Lys Thr Tyr Ile Val
        595                 600
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<210> 50
<211> 556
<212> PRT
<213> Festuca arundinacea

<400> 50

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Asp Pro Phe Arg Ala Ala Leu Ala Pro Ala Ser Pro Pro Leu Glu Ala
1               5                   10                  15
Pro Pro Leu Asp Glu Leu Pro Thr Ala Pro Ser His Ser Glu Pro Ala
            20                  25                  30
Ser Ala Ala Ala Ala Ala Pro Glu Gln Asp Pro Val Asp Leu Gln His
        35                  40                  45
Glu Glu Leu Asp Gly Leu Lys Ala Gly Val Glu Ala Val Arg Ser Arg
    50                  55                  60
Glu Glu Ser Pro Gln Glu Lys Glu Ala Trp Trp Leu Leu Asn Arg Ala
65                  70                  75                  80
Val Val Asn Tyr Cys Gly Ser Ala Val Gly Thr Val Ala Ala Asn Asp
                85                  90                  95
Pro Ser Thr Ala Asn His Met Leu Asn Tyr Asp Gln Val Phe Ile Arg
            100                 105                 110
Asp Phe Val Pro Ser Ala Ile Ala Phe Leu Leu Lys Gly Glu Ser Asp
        115                 120                 125
Ile Val Lys Asn Phe Leu Leu His Thr Leu Gln Leu Gln Ser Trp Glu
    130                 135                 140
Lys Thr Val Asp Cys Tyr Ser Pro Gly Gln Gly Leu Met Pro Ala Ser
145                 150                 155                 160
Phe Lys Val Arg Ser Val Pro Leu Asp Gly Asn Asn Glu Ala Phe Glu
                165                 170                 175
Glu Val Leu Asp Pro Asp Phe Gly Glu Ser Ala Ile Gly Arg Val Ala
            180                 185                 190
Pro Val Asp Ser Gly Leu Trp Trp Ile Ile Leu Leu Arg Ala Tyr Gly
        195                 200                 205
Lys Ile Thr Gly Asp Tyr Ala Leu Gln Glu Arg Val Asp Val Gln Thr
    210                 215                 220
Gly Ile Arg Leu Ile Leu Asn Leu Cys Leu Ser Asp Gly Phe Asp Met
225                 230                 235                 240
Phe Pro Thr Leu Leu Val Thr Asp Gly Ser Cys Met Ile Asp Arg Arg
                245                 250                 255
Met Gly Ile His Gly His Pro Leu Glu Ile Gln Ala Leu Phe Tyr Ser
            260                 265                 270
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Ala Leu Arg Cys Ala Arg Glu Met Val Asn Ile Asp Asp Gly Ser Lys
275 280 285
Asn Leu Ile Arg Val Ile Asn Asn Arg Leu Ser Ala Leu Ser Phe His
290 295 300
Ile Arg Glu Tyr Tyr Trp Val Asp Met Lys Lys Ile Asn Glu Ile Tyr
305 310 315 320
Arg Tyr Lys Thr Glu Glu Tyr Ser His Asp Ala Ile Asn Lys Phe Asn
325 330 335
Ile Tyr Pro Glu Gln Ile Pro Ser Trp Leu Ala Asp Trp Ile Pro Glu
340 345 350
Lys Gly Gly Tyr Leu Ile Gly Asn Leu Gln Pro Ala His Met Asp Phe
355 360 365
Arg Phe Phe Ser Leu Gly Asn Leu Trp Ala Ile Val Ser Ser Leu Ala
370 375 380
Thr Pro Lys Gln Ala Glu Gly Ile Leu Asn Leu Ile Glu Thr Lys Trp
385 390 395 400
Asp Asp Ile Val Ala Asn Met Pro Leu Lys Ile Cys Tyr Pro Ala Leu
405 410 415
Glu Tyr Glu Glu Trp Arg Ile Ile Thr Gly Cys Asp Pro Lys Asn Thr
420 425 430
Pro Trp Ser Tyr His Asn Gly Gly Ser Trp Pro Thr Leu Leu Trp Gln
435 440 445
Phe Thr Leu Ala Cys Ile Lys Met Gly Arg Pro Asp Leu Ala Arg Arg
450 455 460
Ala Val Glu Ala Val Glu Lys Arg Leu Ser Asp Asp Lys Trp Pro Glu
465 470 475 480
Tyr Tyr Asp Thr Arg Asn Gly Arg Phe Ile Gly Lys Gln Ser Arg Leu
485 490 495
Tyr Gln Thr Trp Thr Ile Ala Gly Phe Leu Ser Ser Lys Leu Leu Leu
500 505 510
Asp Cys Pro Glu Met Ala Ser Ile Leu Ile Cys Asp Glu Asp Leu Asp
515 520 525
Leu Leu Glu Gly Cys Ala Cys Gly Ala Asn Lys Ser Ala Arg Val Lys
530 535 540
Cys Ser Arg Arg Ala Ala Arg Ser Gln Val Leu Val
545 550 555

<210> 51
<211> 621
<212> PRT
<213> Festuca arundinacea

<400> 51
Met Ala Ala Ala Ala Ile Ser His Leu Arg Arg Gly Thr Gln Arg His
1 5 10 15
Ala Leu Leu Tyr Leu Ser Arg Arg His Phe Ser Asn Ser Pro Leu Thr
20 25 30
Ala Ala Ala Pro Leu Ala Ala Ala Ala Arg Arg Leu Leu Ser Thr Thr
35 40 45
Val Glu Ser Gly Thr Ser Ser Ala Ala Gly Ser Tyr Lys Pro Pro Pro
50 55 60
Leu Asp Pro Phe Arg Ala Ala Leu Ala Pro Ala Ser Pro Pro Leu Glu
65 70 75 80
Ser Pro Pro Leu Asp Glu Leu Pro Thr Ala Pro Ser His Ser Glu Pro
85 90 95
Ala Ser Ala Ala Ala Ala Ala Pro Glu Gln Asp Pro Val Asp Leu Gln
100 105 110
His Glu Glu Leu Asp Gly Leu Lys Ala Gly Val Glu Ala Val Arg Ser
115 120 125
Arg Glu Glu Ser Pro Gln Glu Lys Glu Ala Trp Trp Leu Leu Asn Arg
130 135 140
Ala Val Val Asn Tyr Cys Gly Ser Ala Val Gly Thr Val Ala Ala Asn
145 150 155 160
Asp Pro Ser Thr Ala Asn His Met Leu Asn Tyr Asp Gln Val Phe Ile
165 170 175
Arg Asp Phe Val Pro Ser Ala Ile Ala Phe Leu Leu Lys Gly Glu Ser
180 185 190
Asp Ile Val Lys Asn Phe Leu Leu His Thr Leu Gln Leu Gln Ser Trp

195 200 205
Glu Lys Thr Val Asp Cys Tyr Ser Pro Gly Gln Gly Leu Met Pro Ala
210 215 220
Ser Phe Lys Val Arg Ser Val Pro Leu Asp Gly Asn Asn Glu Ala Phe
225 230 235 240
Glu Glu Val Leu Asp Pro Asp Phe Gly Glu Ser Ala Ile Gly Arg Val
245 250 255
Ala Pro Val Asp Ser Gly Leu Trp Trp Ile Ile Leu Leu Arg Ala Tyr
260 265 270
Gly Lys Ile Thr Gly Asp Tyr Ala Leu Gln Glu Arg Val Asp Val Gln
275 280 285
Thr Gly Ile Arg Leu Ile Leu Asn Leu Cys Leu Ser Asp Gly Phe Asp
290 295 300
Met Phe Pro Thr Leu Leu Val Thr Asp Gly Ser Cys Met Ile Asp Arg
305 310 315 320
Arg Met Gly Ile His Gly His Pro Leu Glu Ile Gln Ala Leu Phe Tyr
325 330 335
Ser Ala Leu Arg Cys Ala Arg Glu Met Val Asn Ile Asp Asp Gly Ser
340 345 350
Lys Asn Leu Ile Arg Val Ile Asn Asn Arg Leu Ser Ala Leu Ser Phe
355 360 365
His Ile Arg Glu Tyr Tyr Trp Val Asp Met Lys Lys Ile Asn Glu Ile
370 375 380
Tyr Arg Tyr Lys Thr Glu Glu Tyr Ser His Asp Ala Ile Asn Lys Phe
385 390 395 400
Asn Ile Tyr Pro Glu Gln Ile Pro Ser Trp Leu Ala Asp Trp Ile Pro
405 410 415
Glu Lys Gly Gly Tyr Leu Ile Gly Asn Leu Gln Pro Ala His Met Asp
420 425 430
Phe Arg Phe Phe Ser Leu Gly Asn Leu Trp Ala Ile Val Ser Ser Leu
435 440 445
Ala Thr Pro Lys Gln Ala Glu Gly Ile Leu Asn Leu Ile Glu Thr Lys
450 455 460
Trp Asp Asp Ile Val Ala Asn Met Pro Leu Lys Ile Cys Tyr Pro Ala
465 470 475 480
Leu Glu Tyr Glu Glu Trp Arg Ile Ile Thr Gly Cys Asp Pro Lys Asn
485 490 495
Thr Pro Trp Ser Tyr His Asn Gly Gly Ser Trp Pro Thr Leu Leu Trp
500 505 510
Gln Phe Thr Leu Ala Cys Ile Lys Met Gly Arg Pro Asp Leu Ala Arg
515 520 525
Arg Ala Val Glu Ala Val Glu Lys Arg Leu Ser Asp Asp Lys Trp Pro
530 535 540
Glu Tyr Tyr Asp Thr Arg Asn Gly Arg Phe Ile Gly Lys Gln Ser Arg
545 550 555 560
Leu Tyr Gln Thr Trp Thr Ile Ala Gly Phe Leu Ser Ser Lys Leu Leu
565 570 575
Leu Asp Cys Pro Glu Met Ala Ser Ile Leu Ile Cys Asp Glu Asp Leu
580 585 590
Asp Leu Leu Glu Gly Cys Ala Cys Gly Ala Asn Lys Ser Ala Arg Val
595 600 605
Lys Cys Ser Arg Arg Ala Ala Arg Ser Gln Val Leu Val
610 615 620

<210> 52
<211> 244
<212> PRT
<213> Lolium perenne

<400> 52
Leu Leu Glu Lys Arg Lys Leu Asn Glu Ile Tyr Arg Tyr Lys Thr Glu
1 5 10 15
Glu Tyr Ser Tyr Asp Ala Val Asn Lys Phe Asn Ile Tyr Pro Asp Gln
20 25 30
Ile Pro Pro Trp Leu Val Glu Trp Ile Pro Pro Lys Gly Gly Tyr Phe
35 40 45
Ile Gly Asn Leu Gln Pro Ala His Met Asp Phe Arg Phe Phe Ser Leu
50 55 60

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Gly Asn Leu Trp Ser Ile Val Ser Ser Leu Ala Thr Ala Asp Gln Ser
65                  70                  75                  80
His Ala Ile Leu Asp Leu Val Glu Ala Lys Trp Ser Asp Leu Val Ala
                85                  90                  95
Glu Met Pro Met Lys Ile Cys Tyr Pro Ala Leu Glu Asp Gln Glu Trp
            100                 105                 110
Lys Phe Ile Thr Gly Ser Asp Pro Lys Asn Thr Pro Trp Ser Tyr His
        115                 120                 125
Asn Gly Gly Ser Trp Pro Thr Leu Leu Trp Gln Leu Thr Val Ala Cys
    130                 135                 140
Ile Lys Met Asn Arg Pro Glu Ile Ala Ala Arg Ala Val Glu Val Ala
145                 150                 155                 160
Glu Ser Arg Ile Ser Met Asp Lys Trp Pro Glu Tyr Tyr Asp Thr Lys
                165                 170                 175
Arg Gly Arg Phe Ile Gly Lys Gln Ala Arg Leu Phe Gln Thr Trp Ser
            180                 185                 190
Ile Ala Gly Phe Leu Val Ala Lys Leu Leu Leu Glu Asn Pro Glu Lys
        195                 200                 205
Ser Arg Ile Leu Trp Asn Asn Glu Asp Glu Glu Ile Leu Asn Ala Leu
    210                 215                 220
Ser Leu Met Thr Gly Pro Ser Ser Pro Lys Arg Lys Arg Gly Arg Lys
225                 230                 235                 240
Thr Tyr Ile Val


<210> 53
<211> 578
<212> PRT
<213> Lolium perenne

<400> 53
Met Ala Ile Ala Ala Ala Ala Ala Leu Leu Pro Leu His Leu Gly Cys
1               5                   10                  15
Ser Asp Ala Ala Pro Arg Arg Pro Gly Asn Ser Leu Arg Ala His Leu
            20                  25                  30
Arg Lys Gly Gly Ile Arg Gly Arg Arg Arg Ser Pro Pro Cys Ala Val
        35                  40                  45
Asn Ser Leu His Pro Ser Gly Asn Pro Lys Thr Pro Gly Gly Gly Asp
    50                  55                  60
Val Gly Gly Ala Trp Gly Leu Asn Gly Gly Ala Thr Ala Lys Pro Asp
65                  70                  75                  80
His Ala Pro Pro Ser Gln Arg Arg Arg Ala Pro Arg Asp Val Glu Glu
                85                  90                  95
Glu Ala Trp Ala Leu Leu Arg Glu Ser Val Val Ser Tyr Cys Gly Ser
            100                 105                 110
Pro Val Gly Thr Ile Ala Ala Cys Asp Pro Asn Asp Ala Ser Pro Leu
        115                 120                 125
Asn Tyr Asp Gln Val Phe Ile Arg Asp Phe Val Pro Ser Gly Val Ala
    130                 135                 140
Phe Leu Leu Lys Gly Glu His Glu Ile Val Arg Asn Phe Ile Leu His
145                 150                 155                 160
Thr Leu Gln Leu Gln Ser Trp Glu Lys Thr Ile Asp Cys His Ser Pro
                165                 170                 175
Gly Gln Gly Leu Met Pro Ala Ser Phe Lys Val Arg Val Val Pro Leu
            180                 185                 190
Asp Gly Gly Asp Asp Gly Ala Thr Glu Glu Val Leu Asp Pro Asp Phe
        195                 200                 205
Gly Glu Ala Ala Ile Gly Arg Val Ala Pro Val Asp Ser Gly Leu Trp
    210                 215                 220
Trp Ile Ile Leu Leu Arg Ala Tyr Gly Lys Cys Ser Gly Asp Leu Ser
225                 230                 235                 240
Phe His Glu Arg Val Asp Val Gln Thr Gly Ile Lys Leu Ile Leu Lys
                245                 250                 255
Leu Cys Leu Ala Asp Gly Phe Asp Met Phe Pro Thr Leu Leu Val Thr
            260                 265                 270
Asp Gly Ser Cys Met Met Asp Arg Arg Met Gly Ile His Gly His Pro
        275                 280                 285
Leu Glu Ile Gln Ala Leu Phe Tyr Ser Ala Leu Leu Ser Ala Arg Glu
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290 295 300
Met Leu Thr Pro Glu Asp Gly Ser Ala Asp Leu Ile Arg Ala Leu Asn
305 310 315 320
Ser Arg Leu Met Ala Leu Ser Phe His Ile Arg Glu Tyr Tyr Trp Leu
325 330 335
Glu Lys Arg Lys Leu Asn Glu Ile Tyr Arg Tyr Lys Thr Glu Glu Tyr
340 345 350
Ser Tyr Asp Ala Val Asn Lys Phe Asn Ile Tyr Pro Asp Gln Ile Pro
355 360 365
Pro Trp Leu Val Glu Trp Ile Pro Pro Lys Gly Gly Tyr Phe Ile Gly
370 375 380
Asn Leu Gln Pro Ala His Met Asp Phe Arg Phe Phe Ser Leu Gly Asn
385 390 395 400
Leu Trp Ser Ile Val Ser Ser Leu Ala Thr Ala Asp Gln Ser His Ala
405 410 415
Ile Leu Asp Leu Val Glu Ala Lys Trp Ser Asp Leu Val Ala Glu Met
420 425 430
Pro Met Lys Ile Cys Tyr Pro Ala Leu Glu Asp Gln Glu Trp Lys Phe
435 440 445
Ile Thr Gly Ser Asp Pro Lys Asn Thr Pro Trp Ser Tyr His Asn Gly
450 455 460
Gly Ser Trp Pro Thr Leu Leu Trp Gln Leu Thr Val Ala Cys Ile Lys
465 470 475 480
Met Asn Arg Pro Glu Ile Ala Ala Arg Ala Val Glu Val Ala Glu Ser
485 490 495
Arg Ile Ser Met Asp Lys Trp Pro Glu Tyr Tyr Asp Thr Lys Arg Gly
500 505 510
Arg Phe Ile Gly Lys Gln Ala Arg Leu Phe Gln Thr Trp Ser Ile Ala
515 520 525
Gly Phe Leu Val Ala Lys Leu Leu Leu Glu Asn Pro Glu Lys Ser Arg
530 535 540
Ile Leu Trp Asn Asn Glu Asp Glu Glu Ile Leu Asn Ala Leu Ser Leu
545 550 555 560
Met Thr Gly Pro Ser Ser Pro Lys Arg Lys Arg Gly Arg Lys Thr Tyr
565 570 575
Ile Val

<210> 54
<211> 619
<212> PRT
<213> Lolium perenne

<400> 54
Met Asn Gly Gln Thr Thr Met Gly Leu Ala Ala Ala Ala Ala Ala Ala
1 5 10 15
Val Arg Pro Cys Arg Arg Arg Leu Leu Ser Ser Ala Ser Ala Ala Ala
20 25 30
Ala Ala Lys Ala Ser Ala Thr Pro Leu Phe Pro Arg Cys Ser His Pro
35 40 45
Gln His Gln Gln His Ser Arg Arg Ile Pro Phe Leu Val Ser Ala Ala
50 55 60
Ser His Thr Ser Gln Ser Asp Pro Ser Thr Thr Pro Thr Pro Val Thr
65 70 75 80
Ser Asp Pro Arg Ser Ala Val Ala Gly Asn Leu Pro Phe Phe Asp Arg
85 90 95
Val Leu Phe Pro Gly Ser Phe Pro Leu Glu Thr Pro Pro Val Glu Glu
100 105 110
Pro Ala Pro Ala Pro Pro Ala Asp Glu Ala Gln Ala Ser Ala Ser Pro
115 120 125
Val Arg Glu Glu Ser Asp Thr Glu Arg Glu Ala Trp Arg Leu Leu Arg
130 135 140
Arg Ala Val Val Ser Tyr Cys Gly Asp Pro Val Gly Thr Val Ala Ala
145 150 155 160
Glu Asp Pro Glu Cys Thr Glu Met Leu Asn Tyr Asp Gln Val Phe Ile
165 170 175
Arg Asp Phe Val Pro Ser Ala Leu Ala Phe Leu Met Arg Gly Glu Thr
180 185 190

Glu Ile Val Arg Asn Phe Leu Leu His Thr Leu Gln Leu Gln Ser Trp
195 200 205
Glu Lys Thr Val Asp Cys Tyr Ser Pro Gly Gln Gly Leu Met Pro Ala
210 215 220
Ser Phe Lys Ile Lys Thr Val Pro Leu Asp Glu Asn Asn Glu Ala Phe
225 230 235 240
Glu Glu Val Leu Asp Pro Asp Phe Gly Glu Ser Ala Ile Gly Arg Val
245 250 255
Ala Pro Val Asp Ser Gly Leu Trp Trp Ile Ile Leu Leu Arg Ala Tyr
260 265 270
Cys Lys Phe Thr Gly Asp Tyr Ser Leu Gln Glu Arg Val Asp Val Gln
275 280 285
Thr Gly Ile Lys Leu Ile Leu Ser Leu Cys Leu Thr Asp Gly Phe Asp
290 295 300
Met Phe Pro Thr Leu Leu Val Thr Asp Gly Ser Cys Met Ile Asp Arg
305 310 315 320
Arg Met Gly Ile His Gly His Pro Leu Glu Ile Gln Ala Leu Phe Tyr
325 330 335
Ser Ala Leu Arg Cys Ser Arg Glu Met Ile Val Met Asn Asp Gly Ser
340 345 350
Lys His Leu Leu Gln Ala Ile Asn Asn Arg Leu Ser Ala Leu Ser Phe
355 360 365
His Ile Arg Glu Tyr Tyr Trp Val Asp Met Lys Lys Ile Asn Glu Ile
370 375 380
Tyr Arg Tyr Lys Thr Glu Glu Tyr Ser His Asp Ala Thr Asn Lys Phe
385 390 395 400
Asn Ile Tyr Pro Glu Gln Ile Pro Ser Trp Leu Val Asp Trp Val Pro
405 410 415
Glu Lys Gly Gly Tyr Leu Ile Gly Asn Leu Gln Pro Ala His Met Asp
420 425 430
Phe Arg Phe Phe Ser Leu Gly Asn Leu Trp Ala Ile Ser Ser Ser Leu
435 440 445
Thr Thr Pro Thr Gln Ala Glu Gly Ile Leu Ser Leu Ile Glu Glu Lys
450 455 460
Trp Asp Asp Leu Val Ala Asn Met Pro Leu Lys Ile Cys Tyr Pro Ala
465 470 475 480
Met Glu Asp Asp Glu Trp Arg Ile Val Thr Gly Ser Asp Pro Lys Asn
485 490 495
Thr Pro Trp Ser Tyr His Asn Gly Gly Ser Trp Pro Thr Leu Leu Trp
500 505 510
Gln Phe Thr Leu Ala Cys Ile Lys Met Gly Arg Pro Glu Leu Ala Arg
515 520 525
Arg Ala Ile Ala Val Ala Glu Glu Lys Leu Ser Ala Asp Lys Trp Pro
530 535 540
Glu Tyr Tyr Asp Thr Arg Ser Gly Arg Phe Val Gly Lys Gln Ser Arg
545 550 555 560
Ser Tyr Gln Thr Trp Thr Ile Ala Gly Phe Leu Thr Ser Lys Ile Leu
565 570 575
Leu Glu Asn Pro Glu Leu Ala Ser Ile Leu Thr Cys Asp Glu Asp Leu
580 585 590
Glu Leu Leu Glu Gly Cys Ala Cys Cys Leu Ser Lys Arg Thr Arg Cys
595 600 605
Ser Arg Arg Val Thr Lys Ser Asp Ile Ile Gly
610 615

<210> 55
<211> 578
<212> PRT
<213> Lolium perenne

<400> 55
Met Ala Ile Ala Ala Ala Ala Ala Leu Leu Pro Leu His Leu Gly Cys
1 5 10 15
Ser Asp Ala Ala Pro Arg Arg Pro Gly Asn Ser Leu Arg Ala His Leu
20 25 30
Arg Lys Gly Gly Ile Arg Gly Arg Arg Ser Pro Pro Cys Ala Val
35 40 45
Asn Ser Leu His Pro Ser Gly Asn Pro Lys Thr Pro Gly Gly Gly Asp

50 55 60
Val Gly Gly Gly Arg Gly Val Asn Gly Gly Ala Thr Ala Lys Pro Asp
65 70 75 80
His Ala Pro Pro Ser Gln Arg Arg Arg Ala Pro Arg Asp Val Glu Glu
85 90 95
Glu Ala Trp Ala Leu Leu Arg Glu Ser Val Val Ser Tyr Cys Gly Ser
100 105 110
Pro Val Gly Thr Ile Ala Ala Cys Asp Pro Asn Asp Ala Ser Pro Leu
115 120 125
Asn Tyr Asp Gln Val Phe Ile Arg Asp Phe Val Pro Ser Gly Val Ala
130 135 140
Phe Leu Leu Lys Gly Glu His Glu Ile Val Arg Asn Phe Ile Leu His
145 150 155 160
Thr Leu Gln Leu Gln Ser Trp Glu Lys Thr Ile Asp Cys His Ser Pro
165 170 175
Gly Gln Gly Leu Met Pro Ala Ser Phe Lys Val Arg Val Val Pro Leu
180 185 190
Asp Gly Gly Asp Asp Gly Ala Thr Glu Glu Val Leu Asp Pro Asp Phe
195 200 205
Gly Glu Ala Ala Ile Gly Arg Val Ala Pro Val Asp Ser Gly Leu Trp
210 215 220
Trp Ile Ile Leu Leu Arg Ala Tyr Gly Lys Cys Ser Gly Asp Leu Ser
225 230 235 240
Phe His Glu Arg Val Asp Val Gln Thr Gly Ile Lys Leu Ile Leu Lys
245 250 255
Leu Cys Leu Ala Asp Gly Phe Asp Met Phe Pro Thr Leu Leu Val Thr
260 265 270
Asp Gly Ser Cys Met Met Asp Arg Arg Met Gly Ile His Gly His Pro
275 280 285
Leu Glu Ile Gln Ala Leu Phe Tyr Ser Ala Leu Leu Ser Ala Arg Glu
290 295 300
Met Leu Thr Pro Glu Asp Gly Ser Ala Asp Leu Ile Arg Ala Leu Asn
305 310 315 320
Ser Arg Leu Met Ala Leu Ser Phe His Ile Arg Glu Tyr Tyr Trp Leu
325 330 335
Glu Lys Arg Lys Leu Asn Glu Ile Tyr Arg Tyr Lys Thr Glu Glu Tyr
340 345 350
Ser Tyr Asp Ala Val Asn Lys Phe Asn Ile Tyr Pro Asp Gln Ile Pro
355 360 365
Pro Trp Leu Val Glu Trp Ile Pro Pro Lys Gly Gly Tyr Phe Ile Gly
370 375 380
Asn Leu Gln Pro Ala His Met Asp Phe Arg Phe Phe Ser Leu Gly Asn
385 390 395 400
Leu Trp Ser Ile Val Ser Ser Leu Ala Thr Ala Asp Gln Ser His Ala
405 410 415
Ile Leu Asp Leu Val Glu Ala Lys Trp Ser Asp Leu Val Ala Glu Met
420 425 430
Pro Met Lys Ile Cys Tyr Pro Ala Leu Glu Asp Gln Glu Trp Lys Phe
435 440 445
Ile Thr Gly Ser Asp Pro Lys Asn Thr Pro Trp Ser Tyr His Asn Gly
450 455 460
Gly Ser Trp Pro Thr Leu Leu Trp Gln Leu Thr Val Ala Cys Ile Lys
465 470 475 480
Met Asn Arg Pro Glu Ile Ala Ala Arg Ala Val Glu Val Ala Glu Ser
485 490 495
Arg Ile Ser Thr Asp Lys Trp Pro Glu Tyr Tyr Asp Thr Lys Arg Gly
500 505 510
Arg Phe Ile Gly Lys Gln Ala Arg Leu Phe Gln Thr Trp Ser Ile Ala
515 520 525
Gly Phe Leu Val Ala Lys Leu Leu Leu Glu Asn Pro Glu Lys Ser Arg
530 535 540
Ile Leu Trp Asn Asn Glu Asp Glu Glu Ile Leu Asn Ala Leu Ser Leu
545 550 555 560
Met Thr Gly Pro Ser Ser Pro Lys Arg Lys Arg Gly Arg Lys Thr Tyr
565 570 575
Ile Val

<210> 56
<211> 554
<212> PRT
<213> Lolium perenne

<400> 56
Met Lys Arg Val Ser Ser His Val Ser Ile Ala Ser Glu Ala Glu Ile
1 5 10 15
Asn Leu Asp Leu Ser Arg Leu Leu Ile Asp Lys Pro Arg Tyr Thr Leu
20 25 30
Glu Arg Lys Arg Ser Phe Asp Glu Gln Ser Trp Ser Glu Leu Thr His
35 40 45
Thr His Arg Gln Asn Asp Gly Phe Asp Ser Val Leu Gln Ser Pro Ala
50 55 60
Phe Arg Thr Gly Phe Asp Ser Pro Phe Ser Met Gly Thr His Phe Gly
65 70 75 80
Glu Pro Ser Gly Pro His Pro Leu Val Asn Glu Ala Trp Glu Ala Leu
85 90 95
Arg Lys Ser Val Val Tyr Phe Arg Gly Gln Pro Val Gly Thr Ile Ala
100 105 110
Ala Val Asp His Ala Ser Glu Glu Val Leu Asn Tyr Asp Gln Val Phe
115 120 125
Val Arg Asp Phe Val Pro Ser Ala Leu Ala Phe Leu Met Asn Asn Glu
130 135 140
Pro Glu Ile Val Lys Asn Phe Leu Leu Lys Thr Leu His Leu Gln Ser
145 150 155 160
Ser Glu Lys Met Val Asp Arg Phe Lys Leu Gly Ala Gly Ala Met Pro
165 170 175
Ala Ser Phe Lys Val Asp Arg Asn Lys Ser Arg Asn Thr Glu Thr Leu
180 185 190
Val Ala Asp Phe Gly Glu Ser Ala Ile Gly Arg Val Ala Pro Val Asp
195 200 205
Ser Gly Phe Trp Trp Ile Ile Leu Leu Arg Ala Tyr Thr Lys Tyr Thr
210 215 220
Gly Asp Ala Ser Leu Ser Glu Ser Pro Asp Cys Gln Lys Cys Met Arg
225 230 235 240
Leu Ile Leu Asn Leu Cys Leu Ser Glu Gly Phe Asp Thr Phe Pro Thr
245 250 255
Leu Leu Cys Thr Asp Gly Cys Ser Met Ile Asp Arg Arg Met Gly Ile
260 265 270
Tyr Gly Tyr Pro Ile Glu Ile Gln Ala Leu Phe Tyr Met Ala Leu Arg
275 280 285
Cys Ala Leu Gln Met Leu Lys Pro Asp Gly Glu Gly Lys Asp Phe Ile
290 295 300
Glu Lys Ile Gly Gln Arg Leu His Ala Leu Thr Tyr His Met Arg Asn
305 310 315 320
Tyr Phe Trp Leu Asp Phe Pro His Leu Asn Asn Ile Tyr Arg Tyr Lys
325 330 335
Thr Glu Glu Tyr Ser His Thr Ala Val Asn Lys Phe Asn Val Ile Pro
340 345 350
Asp Ser Ile Pro Asp Trp Val Phe Asp Phe Met Pro Cys Arg Gly Gly
355 360 365
Tyr Phe Leu Gly Asn Val Ser Pro Ala Met Met Asp Phe Arg Trp Phe
370 375 380
Ala Leu Gly Asn Cys Ile Ala Ile Ile Ser Ser Leu Ala Thr Pro Glu
385 390 395 400
Gln Ser Ser Ala Ile Met Asp Leu Ile Glu Glu Arg Trp Asp Glu Leu
405 410 415
Val Gly Glu Val Pro Leu Lys Ile Cys Tyr Pro Ala Ile Glu Asn His
420 425 430
Glu Trp Arg Ile Ile Thr Gly Cys Asp Pro Lys Asn Thr Arg Trp Ser
435 440 445
Tyr His Asn Gly Gly Ser Trp Pro Val Leu Leu Trp Leu Leu Thr Ala
450 455 460
Ala Cys Ile Lys Thr Gly Arg Pro Gln Met Ala Lys Arg Ala Ile Glu
465 470 475 480
Leu Ser Glu Ala Arg Leu Leu Lys Asp Gly Trp Pro Glu Tyr Tyr Asp
485 490 495

Gly Lys Leu Gly Lys Phe Val Gly Lys Gln Ala Arg Lys Phe Gln Thr
500 505 510
Trp Ser Ile Ala Gly Tyr Leu Val Ala Arg Met Met Leu Glu Asp Pro
515 520 525
Ser Thr Leu Met Met Ile Ser Met Glu Glu Asp Arg Pro Val Lys Pro
530 535 540
Thr Met Arg Arg Ser Ala Ser Trp Asn Ala
545 550

<210> 57
<211> 552
<212> PRT
<213> Lolium perenne

<400> 57
Met Glu Ala Pro Gly Gly Gly Ala Gly Pro Met Pro Thr Thr Pro Ser
1 5 10 15
His Ala Ser Ile Ala Asp Ser Asp Asp Phe Asp Leu Ser Arg Leu Leu
20 25 30
Asn His Arg Pro Arg Ile Asn Val Glu Arg Gln Arg Ser Phe Asp Asp
35 40 45
Arg Ser Leu Gly Asp Leu Tyr Leu Ser Ala Met Asp Ser Arg Gly Gly
50 55 60
Tyr Met Asp Ser Tyr Asp Ser Met Tyr Ser Pro Gly Gly Gly Leu Arg
65 70 75 80
Ser Leu Thr Gly Thr Pro Ala Ser Ser Thr Arg Leu Ser Phe Glu Pro
85 90 95
Gln Leu Leu Val Ala Glu Ala Trp Glu Ala Leu Arg Arg Ser Leu Val
100 105 110
Cys Phe Arg Gly Glu Pro Leu Gly Thr Ile Ala Ala Val Asp Ser Ser
115 120 125
Ser Asp Glu Val Leu Asn Tyr Asp Gln Val Phe Val Arg Asp Phe Val
130 135 140
Pro Ser Ala Leu Ala Phe Leu Met Asn Gly Glu Pro Asp Ile Val Lys
145 150 155 160
Asn Phe Leu Leu Lys Thr Leu Leu Leu Gln Gly Trp Glu Lys Arg Ile
165 170 175
Asp Arg Phe Lys Leu Gly Glu Gly Ala Met Pro Ala Ser Phe Lys Val
180 185 190
Leu Lys Asp Pro Lys Arg Gly Val Asp Thr Leu Ala Ala Asp Phe Gly
195 200 205
Glu Ser Ala Ile Gly Arg Val Ala Pro Ala Asp Ser Gly Phe Trp Trp
210 215 220
Ile Ile Leu Leu Arg Ala Tyr Thr Lys Ser Thr Gly Asp Leu Thr Leu
225 230 235 240
Ala Glu Thr Pro Glu Cys Gln Lys Gly Ile Arg Leu Ile Met Asn Gln
245 250 255
Cys Leu Ala Glu Gly Phe Asp Thr Phe Pro Thr Leu Leu Cys Ala Asp
260 265 270
Gly Cys Cys Met Ile Asp Arg Arg Met Gly Val Tyr Gly Tyr Pro Ile
275 280 285
Glu Ile Gln Ala Leu Phe Phe Met Ser Leu Arg Cys Ala Leu Leu Leu
290 295 300
Leu Lys Pro Ala Val Glu Gly Asn Ser Ser Ser Lys Asp Asp Asp Ile
305 310 315 320
Met Glu Arg Ile Val Thr Arg Leu His Ala Leu Ser Tyr His Met Arg
325 330 335
Ser Tyr Phe Trp Leu Asp Phe Gln Gln Leu Asn Val Ile Tyr Arg Phe
340 345 350
Lys Thr Glu Glu Tyr Ser His Thr Ala Val Asn Lys Phe Asn Val Ile
355 360 365
Pro Glu Ser Ile Pro Asp Trp Leu Phe Asp Phe Met Pro Ser Arg Gly
370 375 380
Gly Tyr Phe Val Gly Asn Val Ser Pro Ala Arg Met Asp Phe Arg Trp
385 390 395 400
Phe Ala Leu Gly Asn Cys Val Ala Ile Leu Ala Ser Leu Ala Thr Pro
405 410 415
Glu Gln Ala Gly Ala Ile Met Asp Leu Ile Glu Glu Arg Trp Glu Asp

420 425 430
Leu Ile Gly Glu Met Pro Leu Lys Ile Cys Tyr Pro Thr Ile Glu Gly
435 440 445
His Glu Trp Gln Asn Val Thr Gly Cys Asp Pro Lys Asn Thr Arg Trp
450 455 460
Ser Tyr His Asn Gly Gly Ser Trp Pro Val Leu Ile Trp Leu Leu Thr
465 470 475 480
Ala Ala Cys Ile Lys Thr Gly Arg Leu Lys Ile Ala Arg Arg Ala Ile
485 490 495
Asp Leu Ala Glu Ala Arg Leu Gly Lys Asp Gly Trp Pro Glu Tyr Tyr
500 505 510
Asp Gly Lys Leu Gly Arg Tyr Val Gly Lys Gln Ala Arg Lys His Gln
515 520 525
Thr Trp Ser Ile Ala Gly Tyr Leu Val Ala Lys Met Met Leu Glu Asp
530 535 540
Pro Ser His Leu Gly Met Ile Ser
545 550

<210> 58
<211> 562
<212> PRT
<213> Lolium perenne

<400> 58
Met Glu Phe Gly Ala Pro Gly Gly Met Arg Arg Ser Ala Ser His Asn
1 5 10 15
Ser Leu Ser Gly Ser Asp Asp Phe Asp Leu Thr His Leu Leu Asn Lys
20 25 30
Pro Arg Ile Asn Val Glu Arg Gln Arg Ser Phe Asp Asp Arg Ser Leu
35 40 45
Ser Asp Val Ser Tyr Ser Gly Gly Gly His Ala Arg Gly Ala Gly Gly
50 55 60
Gly Phe Asp Gly Met Tyr Ser Pro Gly Gly Gly Leu Arg Ser Leu Val
65 70 75 80
Gly Thr Pro Ala Ser Ser Ala Leu His Ser Phe Glu Pro His Pro Ile
85 90 95
Val Gly Asp Ala Trp Glu Ala Leu Arg Arg Ser Leu Val Phe Phe Arg
100 105 110
Gly Gln Pro Leu Gly Thr Ile Ala Ala Tyr Asp His Ala Ser Glu Glu
115 120 125
Val Leu Asn Tyr Asp Gln Val Phe Val Arg Asp Phe Val Pro Ser Ala
130 135 140
Met Ala Phe Leu Met Asn Gly Glu Pro Glu Ile Val Lys Asn Phe Leu
145 150 155 160
Leu Lys Thr Val Leu Leu Gln Gly Trp Glu Lys Lys Val Asp Arg Phe
165 170 175
Lys Leu Gly Glu Gly Ala Met Pro Ala Ser Phe Lys Val Leu His Asp
180 185 190
Asp Lys Lys Gly Val Asp Thr Leu His Ala Asp Phe Gly Glu Ser Ala
195 200 205
Ile Gly Arg Val Ala Pro Val Asp Ser Gly Phe Trp Trp Ile Ile Leu
210 215 220
Leu Arg Ala Tyr Thr Lys Ser Thr Gly Asp Leu Thr Leu Ala Glu Lys
225 230 235 240
Pro Glu Cys Gln Lys Ala Met Arg Leu Ile Leu Ser Leu Cys Leu Ser
245 250 255
Glu Gly Phe Asp Thr Phe Pro Thr Leu Leu Cys Ala Asp Gly Cys Cys
260 265 270
Met Ile Asp Arg Arg Met Gly Val Tyr Gly Tyr Pro Ile Glu Ile Gln
275 280 285
Ser Leu Phe Phe Met Ala Leu Arg Cys Ala Leu Leu Met Leu Lys His
290 295 300
Asp Asn Glu Gly Lys Asp Phe Val Glu Arg Ile Ala Thr Arg Leu His
305 310 315 320
Ala Leu Ser Tyr His Met Arg Ser Tyr Phe Trp Leu Asp Phe Gln Gln
325 330 335
Leu Asn Asp Ile Tyr Arg Tyr Lys Thr Glu Glu Tyr Ser His Thr Ala
340 345 350

```
Val Asn Lys Phe Asn Val Ile Pro Asp Ser Ile Pro Asp Trp Leu Phe
        355                 360                 365
Asp Phe Met Pro Cys Glu Gly Gly Phe Phe Val Gly Asn Val Ser Pro
    370                 375                 380
Ala Arg Met Asp Phe Arg Trp Phe Ala Leu Gly Asn Met Ile Ala Ile
385                 390                 395                 400
Val Ser Ser Leu Ala Thr Pro Glu Gln Ser Thr Ala Ile Met Asp Leu
                405                 410                 415
Ile Glu Glu Arg Trp Glu Glu Leu Ile Gly Glu Met Pro Leu Lys Ile
            420                 425                 430
Cys Tyr Pro Ala Ile Glu Asn His Glu Trp Arg Ile Val Thr Gly Cys
        435                 440                 445
Asp Pro Lys Asn Thr Arg Trp Ser Tyr His Asn Gly Gly Ser Trp Pro
    450                 455                 460
Val Leu Leu Trp Leu Leu Thr Ala Ala Ser Ile Lys Thr Gly Arg Pro
465                 470                 475                 480
Gln Ile Ala Arg Arg Ala Ile Asp Leu Ala Glu Arg Arg Leu Leu Lys
                485                 490                 495
Asp Gly Trp Pro Glu Tyr Tyr Asp Gly Lys Leu Gly Lys Tyr Val Gly
            500                 505                 510
Lys Gln Ala Arg Lys Phe Gln Thr Trp Ser Ile Ala Gly Tyr Leu Val
        515                 520                 525
Ala Lys Met Leu Leu Glu Asp Pro Ser His Leu Gly Met Ile Ala Leu
    530                 535                 540
Glu Glu Asp Lys Ala Met Lys Pro Val Leu Arg Arg Ser Ala Ser Trp
545                 550                 555                 560
Thr Asn
```

<210> 59
<211> 616
<212> PRT
<213> Lolium perenne

<400> 59

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Met Asp Ser Asp Tyr Gly Val Pro Arg Glu Leu Ser Glu Val Gln Lys
 1               5                  10                  15
Lys Arg Thr Leu Tyr Gln Pro Asp Leu Pro Pro Cys Leu Gln Gly Thr
            20                  25                  30
Thr Val Arg Val Glu Tyr Gly Asp Val Ala Ile Ala Ala Asp Pro Ala
        35                  40                  45
Gly Ala His Val Ile Ser His Ala Phe Pro His Thr Tyr Gly Gln Pro
    50                  55                  60
Leu Ala His Phe Leu Arg Lys Ala Ala Asn Val Ala Asp Ala Lys Val
65                  70                  75                  80
Ile Ser Glu His Pro Ala Val Arg Val Gly Ile Val Phe Cys Gly Arg
                85                  90                  95
Gln Ser Pro Gly Gly His Asn Val Ile Trp Gly Leu His Asp Ala Ile
            100                 105                 110
Lys Ala His Asn Pro Asn Ser Lys Leu Ile Gly Phe Leu Gly Gly Ser
        115                 120                 125
Asp Gly Leu Leu Ala Gln Lys Thr Leu Glu Ile Thr Asp Glu Val Leu
    130                 135                 140
Ser Ser Tyr Lys Asn Gln Gly Gly Tyr Asp Met Leu Gly Arg Thr Lys
145                 150                 155                 160
Asp Gln Ile Arg Thr Thr Glu Gln Val Asn Gly Ala Met Ala Ser Cys
                165                 170                 175
Gln Ala Leu Lys Leu Asp Ala Leu Ile Ile Ile Gly Gly Val Thr Ser
            180                 185                 190
Asn Thr Asp Ala Ala Gln Leu Ala Glu Thr Phe Ala Glu Ala Lys Cys
        195                 200                 205
Ala Thr Lys Val Val Gly Val Pro Val Thr Leu Asn Gly Asp Leu Lys
    210                 215                 220
Asn Gln Phe Val Glu Thr Thr Val Gly Phe Asp Thr Ile Cys Lys Val
225                 230                 235                 240
Asn Ser Gln Leu Ile Ser Asn Met Cys Thr Asp Ala Leu Ser Ala Glu
                245                 250                 255
Lys Tyr Tyr Tyr Phe Ile Arg Met Met Gly Arg Lys Ala Ser His Val
```

```
                260                 265                 270
Ala Leu Glu Cys Ala Leu Gln Ser His Pro Asn Met Val Ile Leu Gly
            275                 280                 285
Glu Glu Val Ala Ala Ser Lys Leu Thr Ile Phe Asp Ile Thr Lys Gln
    290                 295                 300
Ile Cys Asp Ala Val Gln Ala Arg Ala Glu Lys Asp Lys Asn His Gly
305                 310                 315                 320
Val Ile Leu Ile Pro Glu Gly Leu Val Glu Ser Ile Pro Glu Leu Tyr
                325                 330                 335
Ala Leu Leu Gln Glu Ile Asn Gly Leu His Gly Lys Gly Val Ser Ile
            340                 345                 350
Glu Asn Ile Ser Ser Gln Leu Ser Pro Trp Ala Ser Ala Leu Phe Glu
        355                 360                 365
Phe Leu Pro Gln Phe Ile Arg Gln Gln Leu Leu Leu Arg Pro Glu Ser
    370                 375                 380
Asp Asp Ser Ala Gln Leu Ser Gln Ile Glu Thr Glu Lys Leu Leu Ala
385                 390                 395                 400
Gln Leu Val Glu Thr Glu Met Asn Lys Arg Leu Lys Glu Gly Thr Tyr
                405                 410                 415
Lys Gly Lys Lys Phe Asn Ala Ile Cys His Phe Phe Gly Tyr Gln Ala
            420                 425                 430
Arg Gly Ala Met Pro Ser Lys Phe Asp Cys Asp Tyr Ala Tyr Val Leu
        435                 440                 445
Gly His Val Ser Tyr His Ile Leu Ala Ala Gly Leu Asn Gly Tyr Met
    450                 455                 460
Ala Thr Val Thr Asn Leu Lys Ser Pro Leu Asn Lys Trp Arg Cys Gly
465                 470                 475                 480
Ala Ala Pro Ile Ser Ser Met Met Thr Val Lys Arg Trp Ser Arg Gly
                485                 490                 495
Pro Ser Thr Thr Gln Ile Gly Lys Pro Ala Val His Met Ala Ser Val
            500                 505                 510
Asp Leu Arg Gly Lys Ala Tyr Glu Leu Leu Arg Gln Asn Ser Ser Ser
        515                 520                 525
Cys Leu Leu Glu Asp Ile Tyr Arg Asn Pro Gly Pro Leu Gln Phe Glu
    530                 535                 540
Gly Pro Gly Ser Asp Ser Lys Pro Ile Ser Leu Cys Val Glu Asp Gln
545                 550                 555                 560
Asp Tyr Met Gly Arg Ile Lys Lys Leu Gln Glu Tyr Leu Glu Lys Val
                565                 570                 575
Lys Ser Ile Val Lys Pro Gly Cys Ser Gln Asp Val Leu Lys Ala Ala
            580                 585                 590
Leu Ser Ala Met Ser Ser Val Thr Asp Thr Leu Ala Ile Met Thr Ser
        595                 600                 605
Ser Ser Thr Gly Gln Ala Pro Leu
    610                 615
```

<210> 60
<211> 616
<212> PRT
<213> Festuca arundinacea

<400> 60

```
Met Asp Ser Asp Tyr Gly Val Pro Arg Glu Leu Ser Glu Val Gln Lys
 1               5                  10                  15
Lys Arg Thr Leu Tyr Gln Pro Glu Leu Pro Pro Cys Leu Gln Gly Thr
            20                  25                  30
Thr Val Arg Val Glu Tyr Gly Asp Val Ala Ile Ala Ala Asp Pro Ala
        35                  40                  45
Gly Ala His Val Ile Ser His Ala Phe Pro His Thr Tyr Gly Gln Pro
    50                  55                  60
Leu Ala His Phe Leu Arg Lys Ala Ala Asn Val Ala Asp Ala Lys Val
65                  70                  75                  80
Ile Ser Glu His Pro Ala Val Arg Val Gly Ile Val Phe Cys Gly Arg
                85                  90                  95
Gln Ser Pro Gly Gly His Asn Val Ile Trp Gly Leu His Asp Ala Ile
            100                 105                 110
Lys Ala His Asn Ser Asn Ser Lys Leu Ile Gly Phe Leu Gly Gly Ser
        115                 120                 125
```

Asp Gly Leu Leu Ala Gln Lys Thr Leu Glu Ile Thr Asp Glu Val Leu
130 135 140
Ser Ser Tyr Lys Asn Gln Gly Gly Tyr Asp Met Leu Gly Arg Thr Lys
145 150 155 160
Asp Gln Ile Arg Thr Thr Glu Gln Val Asn Gly Ala Met Ala Ser Cys
165 170 175
Gln Asp Leu Lys Leu Asp Ala Leu Ile Ile Ile Gly Gly Val Thr Ser
180 185 190
Asn Thr Asp Ala Ala Gln Leu Ala Glu Thr Phe Ala Glu Ala Lys Cys
195 200 205
Ala Thr Lys Val Val Gly Val Pro Val Thr Leu Asn Gly Asp Leu Lys
210 215 220
Asn Gln Phe Val Glu Thr Thr Val Gly Phe Asp Thr Ile Cys Lys Val
225 230 235 240
Asn Ser Gln Leu Ile Ser Asn Met Cys Thr Asp Ala Leu Ser Ala Glu
245 250 255
Lys Tyr Tyr Tyr Phe Ile Arg Met Met Gly Arg Lys Ala Ser His Val
260 265 270
Ala Leu Glu Cys Ala Leu Gln Ser His Pro Asn Met Val Ile Leu Gly
275 280 285
Glu Glu Val Ala Ala Ser Lys Leu Thr Ile Phe Asp Ile Thr Lys Gln
290 295 300
Ile Cys Asp Ala Val Gln Ala Arg Ala Glu Lys Asp Lys Asn His Gly
305 310 315 320
Val Ile Leu Ile Pro Glu Gly Leu Val Glu Ser Ile Pro Glu Leu Tyr
325 330 335
Ala Leu Leu Gln Glu Ile Asn Gly Leu His Gly Lys Gly Val Ser Ile
340 345 350
Glu Asn Ile Ser Ser Gln Leu Ser Pro Trp Ala Ser Ala Leu Phe Glu
355 360 365
Phe Leu Pro Gln Phe Ile Arg His Gln Leu Leu Leu Arg Pro Glu Ser
370 375 380
Asp Asp Ser Ala Gln Leu Ser Gln Ile Glu Thr Glu Lys Leu Leu Ala
385 390 395 400
Gln Leu Val Glu Thr Glu Met Asn Lys Arg Leu Lys Glu Gly Thr Tyr
405 410 415
Lys Gly Lys Lys Phe Asn Ala Ile Cys His Phe Phe Gly Tyr Gln Ala
420 425 430
Arg Gly Ala Met Pro Ser Lys Phe Asp Cys Asp Tyr Ala Tyr Val Leu
435 440 445
Gly His Val Ser Tyr His Ile Leu Ala Ala Gly Leu Asn Gly Tyr Met
450 455 460
Ala Thr Val Thr Asn Leu Lys Ser Pro Leu Asn Lys Trp Arg Cys Gly
465 470 475 480
Ala Ala Pro Ile Ser Ser Met Met Thr Val Lys Arg Trp Ser Arg Gly
485 490 495
Pro Ser Thr Thr Gln Ile Gly Lys Pro Ala Met His Met Ala Thr Val
500 505 510
Asp Leu Arg Gly Lys Ala Tyr Glu Leu Leu Arg Gln Asn Ser Ser Ser
515 520 525
Tyr Leu Leu Glu Asp Ile Tyr Arg Asn Pro Gly Pro Leu Gln Phe Glu
530 535 540
Gly Pro Gly Ala Asp Ser Lys Pro Ile Ser Leu Cys Val Glu Asp Gln
545 550 555 560
Asp Tyr Met Gly Arg Ile Lys Lys Leu Gln Glu Tyr Leu Glu Lys Val
565 570 575
Lys Ser Ile Val Lys Pro Gly Cys Ser Gln Asp Val Leu Lys Ala Ala
580 585 590
Leu Ser Ala Met Ser Ser Val Thr Glu Thr Leu Ala Ile Met Thr Ser
595 600 605
Ser Ser Thr Gly Gln Ala Pro Leu
610 615

<210> 61
<211> 563
<212> PRT
<213> Lolium perenne

<400> 61
Met Ala Ala Ala Ala Val Ala Thr Ser Asn Gly Ala Ser Ala Asn Gly
1   5   10   15
Pro Thr Pro Gly Arg Leu Ala Ser Val Tyr Ser Glu Val Gln Thr Ser
            20   25   30
Arg Ile Ala His Ala Leu Pro Leu Pro Ser Val Leu Arg Ser His Phe
        35   40   45
Thr Leu Ala Asp Gly Ala Ala Ser Ser Ala Thr Gly Asn Pro Glu Glu
    50   55   60
Ile Ala Lys Leu Phe Pro Asn Leu Tyr Gly Gln Pro Ser Ala Ala Val
65   70   75   80
Val Pro Ser Ala Gln Pro Val Ala Thr Lys Pro Leu Lys Ile Gly Val
                85   90   95
Val Leu Ser Gly Gly Gln Ala Pro Gly Gly His Asn Val Ile Cys Gly
            100   105   110
Ile Phe Asp Tyr Leu Gln Glu Arg Ala Lys Gly Ser Thr Met Tyr Gly
        115   120   125
Phe Lys Gly Gly Pro Ala Gly Val Met Lys Gly Lys Tyr Val Glu Leu
    130   135   140
Asn Ala Asp Phe Val Tyr Pro Tyr Arg Asn Gln Gly Gly Phe Asp Met
145   150   155   160
Ile Cys Ser Gly Arg Asp Lys Ile Glu Thr Pro Glu Gln Phe Lys Gln
                165   170   175
Ala Glu Asp Thr Val Thr Lys Leu Asp Leu Asp Gly Leu Val Val Ile
            180   185   190
Gly Gly Asp Asp Ser Asn Thr Asn Ala Cys Leu Leu Gly Glu Tyr Phe
        195   200   205
Arg Gly Arg Asn Leu Lys Thr Arg Val Ile Gly Cys Pro Lys Thr Ile
    210   215   220
Asp Gly Asp Leu Lys Cys Lys Glu Val Pro Thr Ser Phe Gly Phe Asp
225   230   235   240
Thr Ala Cys Lys Ile Tyr Ser Glu Met Ile Gly Asn Val Met Thr Asp
                245   250   255
Ala Arg Ser Thr Gly Lys Tyr Tyr His Phe Val Arg Leu Met Gly Arg
            260   265   270
Ala Ala Ser His Ile Thr Leu Glu Cys Ala Leu Gln Thr His Pro Asn
        275   280   285
Val Ser Leu Ile Gly Glu Glu Val Ala Glu Lys Lys Glu Thr Leu Lys
    290   295   300
Gln Val Thr Asp Tyr Ile Thr Asp Val Ile Cys Lys Arg Ala Glu Leu
305   310   315   320
Gly Tyr Asn Tyr Gly Val Ile Leu Ile Pro Glu Gly Leu Ile Asp Phe
                325   330   335
Ile Pro Glu Val Gln Lys Leu Ile Ala Glu Leu Asn Glu Ile Leu Ala
            340   345   350
His Asp Val Val Asp Glu Ala Gly Ala Trp Lys Ser Lys Leu Gln Pro
        355   360   365
Glu Ser Arg Gln Leu Phe Asp Phe Leu Pro Asn Thr Ile Gln Glu Gln
    370   375   380
Leu Leu Leu Glu Arg Asp Pro His Gly Asn Val Gln Val Ala Lys Ile
385   390   395   400
Glu Thr Glu Lys Met Leu Ile Ala Met Val Glu Thr Glu Leu Glu Lys
                405   410   415
Arg Arg Ser Ala Gly Lys Tyr Ser Ala His Phe Arg Gly Gln Ser His
            420   425   430
Phe Phe Gly Tyr Glu Gly Arg Cys Gly Leu Pro Thr Asn Phe Asp Ser
        435   440   445
Ser Tyr Cys Tyr Ala Leu Gly Tyr Gly Ala Gly Ala Leu Leu Gln Phe
    450   455   460
Gly Lys Thr Gly Leu Ile Ser Ser Val Gly Asn Leu Ala Ala Pro Val
465   470   475   480
Glu Glu Trp Thr Val Gly Gly Thr Pro Leu Thr Ala Leu Met Asp Val
                485   490   495
Glu Arg Arg His Gly Lys Phe Lys Pro Val Ile Lys Lys Ala Met Val
            500   505   510
Glu Leu Asp Ala Ala Pro Phe Lys Lys Phe Ala Ser Met Arg Asp Glu
        515   520   525
Trp Ala Ile Lys Asn Arg Tyr Ile Ser Pro Gly Pro Ile Gln Phe Ser

```
    530                 535                     540
Gly Pro Gly Ser Asp Ala Ser Asn His Thr Leu Met Leu Glu Leu Gly
545                 550                 555                     560
Ala Gln Thr


<210> 62
<211> 563
<212> PRT
<213> Lolium perenne

<400> 62
Met Ala Ala Ala Ala Val Ala Thr Ser Asn Gly Ala Ser Ala Asn Gly
 1               5                  10                  15
Pro Thr Pro Gly Arg Leu Ala Ser Val Tyr Ser Glu Val Gln Thr Ser
            20                  25                  30
Arg Ile Ala His Ala Leu Pro Leu Pro Ser Val Leu Arg Ser His Phe
        35                  40                  45
Thr Leu Ala Asp Gly Ala Ala Ser Ser Ala Thr Gly Asn Pro Glu Glu
    50                  55                  60
Ile Ala Lys Leu Phe Pro Asn Leu Tyr Gly Gln Pro Ser Ala Ala Val
65                  70                  75                  80
Val Pro Ser Ala Gln Pro Val Ala Thr Lys Pro Leu Lys Ile Gly Val
                85                  90                  95
Val Leu Ser Gly Gly Gln Ala Pro Gly Gly His Asn Val Ile Cys Gly
            100                 105                 110
Ile Phe Asp Tyr Leu Gln Glu Arg Ala Lys Gly Ser Thr Met Tyr Gly
        115                 120                 125
Phe Lys Gly Gly Pro Ala Gly Val Met Lys Gly Lys Tyr Val Glu Leu
    130                 135                 140
Asn Ala Asp Phe Val Tyr Pro Tyr Arg Asn Gln Gly Gly Phe Asp Met
145                 150                 155                 160
Ile Cys Ser Gly Arg Asp Lys Ile Glu Thr Pro Glu Gln Phe Lys Gln
                165                 170                 175
Ala Glu Asp Thr Val Thr Lys Leu Asp Leu Asp Gly Leu Val Val Ile
            180                 185                 190
Gly Gly Asp Asp Ser Asn Thr Asn Ala Cys Leu Leu Gly Glu Tyr Phe
        195                 200                 205
Arg Gly Arg Asn Leu Lys Thr Arg Val Ile Gly Cys Pro Lys Thr Ile
    210                 215                 220
Asp Gly Asp Leu Lys Cys Lys Glu Val Pro Thr Ser Phe Gly Phe Asp
225                 230                 235                 240
Thr Ala Cys Lys Ile Tyr Ser Glu Met Ile Gly Asn Val Met Thr Asp
                245                 250                 255
Ala Arg Ser Thr Gly Lys Tyr Tyr His Phe Val Arg Leu Met Gly Arg
            260                 265                 270
Ala Ala Ser His Ile Thr Leu Glu Cys Ala Leu Gln Thr His Pro Asn
        275                 280                 285
Val Ser Leu Ile Gly Glu Glu Val Ala Glu Lys Lys Glu Thr Leu Lys
    290                 295                 300
Gln Val Thr Asp Tyr Ile Thr Asp Val Ile Cys Lys Arg Ala Glu Leu
305                 310                 315                 320
Gly Tyr Asn Tyr Gly Val Ile Leu Ile Pro Glu Gly Leu Ile Asp Phe
                325                 330                 335
Ile Pro Glu Val Gln Lys Leu Ile Ala Glu Leu Asn Glu Ile Leu Ala
            340                 345                 350
His Asp Val Val Asp Glu Ala Gly Ala Trp Lys Ser Lys Leu Gln Pro
        355                 360                 365
Glu Ser Arg Gln Leu Phe Asp Phe Leu Pro Asn Thr Ile Gln Glu Gln
    370                 375                 380
Leu Leu Leu Glu Arg Asp Pro His Gly Asn Val Gln Val Ala Lys Ile
385                 390                 395                 400
Glu Thr Glu Lys Met Leu Ile Ala Met Val Glu Thr Glu Leu Glu Lys
                405                 410                 415
Arg Arg Ser Ala Gly Lys Tyr Ser Ala His Phe Arg Gly Gln Ser His
            420                 425                 430
Phe Phe Gly Tyr Glu Gly Arg Cys Gly Leu Pro Thr Asn Phe Asp Ser
        435                 440                 445
```

Ser Tyr Cys Tyr Ala Leu Gly Tyr Gly Ala Gly Ala Leu Leu Gln Phe
450 455 460
Gly Lys Thr Gly Leu Ile Ser Ser Val Gly Asn Leu Ala Ala Pro Val
465 470 475 480
Glu Glu Trp Thr Val Gly Gly Thr Pro Leu Thr Ala Leu Met Asp Val
485 490 495
Glu Arg Arg His Gly Lys Phe Lys Pro Val Ile Lys Lys Ala Met Val
500 505 510
Glu Leu Asp Ala Ala Pro Phe Lys Lys Phe Ala Ser Met Arg Asp Glu
515 520 525
Trp Ala Ile Lys Asn Arg Tyr Ile Ser Pro Gly Pro Ile Gln Phe Ser
530 535 540
Gly Pro Gly Ser Asp Ala Ser Asn His Thr Leu Met Leu Glu Leu Gly
545 550 555 560
Ala Gln Thr

<210> 63
<211> 563
<212> PRT
<213> Festuca arundinacea

<400> 63
Met Ala Ala Ala Ala Val Ala Thr Ser Asn Gly Ala Ser Ala Asn Gly
1 5 10 15
Pro Thr Pro Gly Arg Leu Ala Ser Val Tyr Ser Glu Val Gln Thr Ser
20 25 30
Arg Ile Ala His Ala Leu Pro Leu Pro Ser Val Leu Arg Ser Asn Phe
35 40 45
Thr Leu Ala Asp Gly Pro Ala Ser Ser Ala Thr Gly Asn Pro Glu Glu
50 55 60
Ile Ala Lys Leu Phe Pro Asn Leu Tyr Gly Gln Pro Ser Ala Ala Val
65 70 75 80
Val Pro Ser Ala Glu Pro Val Pro Thr Lys Pro Leu Lys Ile Gly Val
85 90 95
Val Leu Ser Gly Gly Gln Ala Pro Gly Gly His Asn Val Ile Cys Gly
100 105 110
Ile Phe Asp Tyr Leu Gln Glu Arg Ala Lys Gly Ser Thr Met Tyr Gly
115 120 125
Phe Lys Gly Gly Pro Ala Gly Ile Met Lys Gly Lys Tyr Ile Glu Leu
130 135 140
Asn Ala Asp Phe Val Tyr Pro Tyr Arg Asn Gln Gly Gly Phe Asp Met
145 150 155 160
Ile Cys Ser Gly Arg Asp Lys Ile Glu Thr Pro Glu Gln Phe Lys Gln
165 170 175
Ala Glu Asp Thr Val Asn Lys Leu Asp Leu Asp Gly Leu Val Val Ile
180 185 190
Gly Gly Asp Asp Ser Asn Thr Asn Ala Cys Leu Leu Gly Glu Tyr Phe
195 200 205
Arg Gly Arg Asn Leu Lys Thr Arg Val Ile Gly Cys Pro Lys Thr Ile
210 215 220
Asp Gly Asp Leu Lys Cys Lys Glu Val Pro Ile Ser Phe Gly Phe Asp
225 230 235 240
Thr Ala Cys Lys Ile Tyr Ser Glu Met Ile Gly Asn Val Met Thr Asp
245 250 255
Ala Arg Ser Thr Gly Lys Tyr Tyr His Phe Val Arg Leu Met Gly Arg
260 265 270
Ala Ala Ser His Ile Thr Leu Glu Cys Ala Leu Gln Thr His Pro Asn
275 280 285
Val Ser Leu Ile Gly Glu Glu Val Ala Glu Lys Lys Glu Thr Leu Lys
290 295 300
Gln Val Thr Asp Tyr Ile Thr Asp Val Ile Cys Lys Arg Ala Glu Leu
305 310 315 320
Gly Tyr Asn Tyr Gly Val Ile Leu Ile Pro Glu Gly Leu Ile Asp Phe
325 330 335
Ile Pro Glu Val Gln Lys Leu Ile Ala Glu Leu Asn Glu Ile Leu Ala
340 345 350
His Asp Val Val Asp Glu Ala Gly Ala Trp Lys Ser Lys Leu Gln Pro

```
                355                     360                     365
Glu Ser Arg Gln Leu Phe Asp Phe Leu Pro Asn Thr Ile Gln Glu Gln
    370                     375                     380
Leu Leu Leu Glu Arg Asp Pro His Gly Asn Val Gln Val Ala Lys Ile
385                     390                     395                 400
Glu Thr Glu Lys Met Leu Ile Ala Met Val Glu Thr Glu Leu Glu Lys
                405                     410                     415
Arg Arg Ala Ala Gly Lys Tyr Ser Ala His Phe Arg Gly Gln Ser His
            420                     425                     430
Phe Phe Gly Tyr Glu Gly Arg Cys Gly Leu Pro Thr Asn Phe Asp Ser
        435                     440                     445
Ser Tyr Cys Tyr Ala Leu Gly Tyr Gly Ala Gly Ala Leu Leu Gln Phe
    450                     455                     460
Gly Lys Thr Gly Leu Ile Ser Ser Val Gly Asn Leu Ala Ala Pro Val
465                     470                     475                 480
Glu Glu Trp Thr Val Gly Gly Thr Pro Leu Thr Ala Leu Met Asp Val
                485                     490                     495
Glu Arg Arg His Gly Lys Phe Lys Pro Val Ile Lys Lys Ala Met Val
            500                     505                     510
Glu Leu Asp Ala Ala Pro Phe Lys Lys Phe Ala Ser Met Arg Asp Glu
        515                     520                     525
Trp Ala Ile Lys Asn Arg Tyr Ile Ser Pro Gly Pro Ile Gln Phe Ser
    530                     535                     540
Gly Pro Gly Ser Asp Ala Ser Asn His Thr Leu Met Leu Glu Leu Gly
545                     550                     555                 560
Ala Gln Ile
```

<210> 64
<211> 964
<212> PRT
<213> Lolium perenne

<400> 64

```
Met Val Gly Asn Asp Asn Trp Ile Asn Ser Tyr Leu Asp Ala Ile Leu
 1               5                  10                  15
Asp Ala Gly Lys Ser Ser Ile Gly Gly Asp Arg Pro Ser Leu Leu Leu
            20                  25                  30
Arg Glu Arg Gly His Phe Ser Pro Ala Arg Tyr Phe Val Glu Glu Val
        35                  40                  45
Ile Thr Gly Tyr Asp Glu Thr Asp Leu Tyr Lys Thr Trp Leu Arg Ala
    50                  55                  60
Asn Ala Met Arg Ser Pro Gln Glu Arg Asn Thr Arg Leu Glu Asn Met
65                  70                  75                  80
Thr Trp Arg Ile Trp Asn Leu Ala Arg Lys Lys Lys Glu Leu Glu Lys
                85                  90                  95
Glu Glu Ala Cys Arg Leu Leu Lys Arg His Pro Glu Thr Glu Lys Thr
            100                 105                 110
Arg Thr Asp Ala Thr Ala Asp Met Ser Glu Asp Leu Phe Asp Gly Glu
        115                 120                 125
Lys Gly Glu Asp Ala Gly Asp Pro Ser Val Ala Tyr Gly Asp Ser Thr
    130                 135                 140
Thr Gly Ser Ser Pro Lys Thr Ser Ser Val Asp Lys Leu Tyr Ile Val
145                 150                 155                 160
Leu Ile Ser Leu His Gly Leu Val Arg Gly Glu Asn Met Glu Leu Gly
                165                 170                 175
Arg Asp Ser Asp Thr Gly Gly Gln Val Lys Tyr Val Val Glu Phe Ala
            180                 185                 190
Lys Ala Leu Ser Ser Ser Pro Gly Val Tyr Arg Val Asp Leu Leu Thr
        195                 200                 205
Arg Gln Ile Val Ala Pro Asn Phe Asp Arg Ser Tyr Gly Glu Pro Glu
    210                 215                 220
Glu Met Leu Val Ser Thr Thr Phe Lys Asn Ser Lys His Glu Arg Gly
225                 230                 235                 240
Val Asn Ser Gly Gly Tyr Ile Ile Arg Ile Pro Phe Gly Pro Lys Asp
                245                 250                 255
Lys Tyr Leu Ala Lys Glu His Met Trp Pro Phe Ile Gln Asp Phe Val
            260                 265                 270
```

```
Asp Gly Ala Leu Ser His Ile Leu Arg Met Ser Lys Thr Ile Gly Glu
        275                 280                 285
Glu Ile Gly Cys Gly His Pro Val Trp Pro Ala Val Ile His Gly His
    290                 295                 300
Tyr Ala Ser Ala Gly Val Ala Ala Ala Leu Leu Ser Gly Ala Leu Asn
305                 310                 315                 320
Leu Pro Met Ala Phe Thr Gly His Phe Leu Gly Lys Asp Lys Leu Glu
                325                 330                 335
Gly Leu Leu Lys Gln Gly Arg Gln Ser Arg Glu Gln Ile Asn Met Thr
            340                 345                 350
Tyr Lys Ile Met Arg Arg Ile Glu Ala Glu Glu Leu Ser Leu Asp Ala
        355                 360                 365
Ser Glu Ile Val Ile Ala Ser Thr Arg Gln Glu Ile Glu Glu Gln Trp
    370                 375                 380
Asn Leu Tyr Asp Gly Phe Glu Val Ile Leu Ala Arg Lys Leu Arg Ala
385                 390                 395                 400
Arg Val Lys Arg Gly Ala Asn Cys Tyr Gly Arg Tyr Met Pro Arg Met
                405                 410                 415
Val Ile Ile Pro Pro Gly Val Glu Phe Gly His Val Val His Asp Phe
            420                 425                 430
Asp Met Asp Gly Glu Glu Glu Asn His Gly Pro Ala Ser Glu Asp Pro
        435                 440                 445
Pro Ile Trp Ser Gln Ile Met Arg Phe Phe Thr Asn Pro Arg Lys Pro
    450                 455                 460
Met Ile Leu Ala Val Ala Arg Pro Tyr Pro Glu Lys Asn Ile Thr Ser
465                 470                 475                 480
Leu Val Lys Ala Phe Gly Glu Cys Arg Pro Leu Arg Glu Leu Ala Asn
                485                 490                 495
Leu Thr Leu Ile Met Gly Asn Arg Glu Ala Ile Ser Lys Met His Asn
            500                 505                 510
Thr Ser Ala Ser Val Leu Thr Ser Val Leu Thr Leu Ile Asp Glu Tyr
        515                 520                 525
Asp Leu Tyr Gly Gln Val Ala Tyr Pro Lys His His Lys His Ser Glu
    530                 535                 540
Val Pro Asp Ile Tyr Arg Leu Ala Thr Arg Thr Lys Gly Ala Phe Val
545                 550                 555                 560
Asn Val Ala Tyr Phe Glu Gln Phe Gly Val Thr Leu Ile Glu Ala Ala
                565                 570                 575
Met Asn Gly Leu Pro Val Ile Ala Thr Lys Asn Gly Ala Pro Val Glu
            580                 585                 590
Ile Asn Gln Val Leu Asn Asn Gly Leu Leu Val Asp Pro His Asp Gln
        595                 600                 605
Asn Ala Ile Ala Asp Ala Leu Tyr Lys Leu Leu Ser Glu Lys Gln Leu
    610                 615                 620
Trp Ser Arg Cys Arg Glu Asn Gly Leu Lys Asn Ile His Gln Phe Ser
625                 630                 635                 640
Trp Pro Glu His Cys Lys Asn His Leu Ser Arg Ile Leu Thr Leu Gly
                645                 650                 655
Ala Arg Ser Pro Ala Ile Gly Ser Lys Glu Glu Arg Ser Asn Ala Pro
            660                 665                 670
Ile Ser Gly Arg Lys His Ile Ile Val Ile Ser Val Asp Ser Val Asn
        675                 680                 685
Lys Glu Asp Leu Val Arg Ile Ile Arg Asn Ala Ile Glu Ala Ala His
    690                 695                 700
Thr Gln Asn Thr Pro Ala Ser Thr Gly Phe Val Leu Ser Thr Ser Leu
705                 710                 715                 720
Thr Leu Ser Glu Ile Cys Ser Leu Leu Val Ser Val Gly Met His Pro
                725                 730                 735
Ala Gly Phe Asp Ala Phe Ile Cys Asn Ser Gly Ser Ser Ile Tyr Tyr
            740                 745                 750
Pro Ser Tyr Ser Gly Asn Thr Pro Ser Ser Ser Lys Val Thr His Val
        755                 760                 765
Ile Asp Gln Asn His Gln Ser His Ile Glu Tyr Arg Trp Gly Gly Glu
    770                 775                 780
Gly Leu Arg Lys Tyr Leu Val Lys Trp Ala Thr Ser Val Val Glu Arg
785                 790                 795                 800
Lys Gly Arg Ile Glu Arg Gln Met Ile Phe Glu Asp Ser Glu His Ser
                805                 810                 815
```

```
Ser Thr Tyr Cys Leu Ala Phe Lys Val Val Asn Pro Asn His Leu Pro
            820                 825                 830
Pro Leu Lys Glu Leu Arg Lys Leu Met Arg Ile Gln Ser Leu Arg Cys
        835                 840                 845
Asn Ala Leu Tyr Asn His Ser Ala Thr Arg Leu Ser Val Thr Pro Ile
    850                 855                 860
His Ala Ser Arg Ser Gln Ala Ile Arg Tyr Leu Phe Ile Arg Trp Gly
865                 870                 875                 880
Ile Glu Leu Pro Asn Ile Val Val Leu Val Gly Glu Ser Gly Asp Ser
                885                 890                 895
Asp Tyr Glu Glu Leu Leu Gly Gly Leu His Arg Thr Ile Ile Leu Lys
            900                 905                 910
Gly Asp Phe Asn Ile Ala Ala Asn Arg Ile His Thr Val Arg Arg Tyr
        915                 920                 925
Pro Leu Gln Asp Val Val Ala Leu Asp Ser Ser Asn Ile Ile Glu Val
    930                 935                 940
Glu Gly Cys Thr Thr Asp Val Ile Lys Ser Ala Leu Arg Gln Ile Gly
945                 950                 955                 960
Val Pro Thr Gln
```

<210> 65
<211> 984
<212> PRT
<213> Festuca arundinacea

<220>
<221> VARIANT
<222> (1)...(984)
<223> Xaa = Any Amino Acid

<400> 65

```
Met Val Gly Gly Met Cys Gly Asn Asp Asn Trp Ile Asn Ser Tyr Leu
 1               5                  10                  15
Asp Ala Ile Leu Asp Ala Gly Lys Gly Ala Pro Gly Gly Gly Ala Gly
            20                  25                  30
Pro Gly Gly Gly Arg Gly Gly Gly Gly Gly Gly Ala Gly Asp Arg Pro
        35                  40                  45
Ser Leu Leu Leu Arg Glu Arg Gly His Phe Ser Pro Ala Arg Tyr Phe
    50                  55                  60
Val Glu Glu Val Ile Thr Gly Tyr Asp Glu Thr Asp Leu Tyr Lys Thr
65                  70                  75                  80
Trp Ser Arg Ala Asn Ala Met Arg Ser Pro Gln Glu Arg Asn Thr Arg
                85                  90                  95
Leu Glu Asn Met Thr Trp Arg Ile Trp Asn Leu Ala Arg Lys Lys Lys
            100                 105                 110
Glu Xaa Glu Ala Glu Glu Ala Asn Arg Leu Leu Lys Arg Arg Leu Glu
        115                 120                 125
Thr Glu Lys Pro Arg Thr Asp Ala Ala Ala Glu Met Ser Glu Asp Leu
    130                 135                 140
Phe Glu Gly Gln Lys Gly Glu Asp Ala Gly Asp Ala Ser Val Ala Tyr
145                 150                 155                 160
Gly Asp Ser Ser Ala Ser Asn Thr Pro Arg Ile Ser Ser Ile Asp Lys
                165                 170                 175
Leu Tyr Ile Val Leu Ile Ser Leu His Gly Leu Val Arg Gly Glu Asn
            180                 185                 190
Met Glu Leu Gly Arg Asp Ser Asp Thr Ser Gly Gln Val Lys Tyr Val
        195                 200                 205
Val Glu Leu Ala Lys Ala Leu Ser Ser Cys Pro Gly Val Tyr Arg Val
    210                 215                 220
Asp Leu Leu Thr Arg Gln Ile Leu Ala Pro Asn Tyr Asp Arg Gly Tyr
225                 230                 235                 240
Gly Glu Pro Ser Glu Thr Leu Leu Pro Thr Asn Leu Lys Asn Phe Lys
                245                 250                 255
His Glu Arg Gly Glu Asn Ser Gly Ala Tyr Ile Thr Arg Ile Pro Phe
            260                 265                 270
Gly Pro Lys Asp Lys Tyr Leu Ala Lys Glu Gln Leu Trp Pro Tyr Val
        275                 280                 285
```

Gln Glu Phe Val Asp Gly Ala Leu Ser His Ile Val Arg Met Ser Lys
290 295 300
Thr Ile Gly Glu Glu Ile Gly Cys Gly His Pro Met Trp Pro Ala Ala
305 310 315 320
Ile His Gly His Tyr Ala Ser Ala Gly Val Ala Ala Ala Leu Leu Ser
325 330 335
Gly Ala Leu Asn Val His Met Ile Phe Thr Gly His Phe Leu Gly Arg
340 345 350
Asp Lys Leu Glu Gly Leu Leu Lys Gln Gly Lys Gln Thr Arg Glu Glu
355 360 365
Ile Asn Met Thr Tyr Lys Ile Met Arg Arg Ile Glu Ala Glu Glu Leu
370 375 380
Ser Leu Asp Ala Ser Glu Ile Val Ile Ala Ser Thr Arg Gln Glu Ile
385 390 395 400
Glu Glu Gln Trp Asn Leu Tyr Asp Gly Phe Glu Val Met Leu Ala Arg
405 410 415
Lys Leu Arg Ala Arg Val Lys Arg Gly Ala Asn Cys Tyr Gly Arg Tyr
420 425 430
Met Pro Arg Met Val Ile Ile Pro Pro Gly Val Glu Phe Gly His Met
435 440 445
Ile Gln Asp Phe Asp Met Asp Gly Glu Glu Asp Ser Pro Ser Pro Ala
450 455 460
Ser Glu Asp Pro Pro Ile Trp Ser Glu Ile Met Arg Phe Phe Thr Asn
465 470 475 480
Pro Arg Lys Pro Leu Ile Leu Ala Val Ala Arg Pro Tyr Pro Glu Lys
485 490 495
Asn Ile Thr Thr Leu Val Arg Ala Phe Gly Glu Cys Arg Pro Leu Arg
500 505 510
Glu Leu Ala Asn Leu Thr Leu Ile Met Gly Asn Arg Glu Ala Ile Ser
515 520 525
Lys Met Ser Asn Met Ser Ala Ala Val Leu Thr Ser Val Leu Thr Leu
530 535 540
Ile Asp Glu Tyr Asp Leu Tyr Gly Gln Val Ala Tyr Pro Lys His His
545 550 555 560
Lys His Ser Glu Val Leu Asp Ile Tyr Arg Leu Ala Ala Arg Thr Lys
565 570 575
Gly Ala Phe Val Asn Val Ala Tyr Phe Glu Gln Phe Gly Val Thr Leu
580 585 590
Ile Glu Ala Ala Met His Gly Leu Pro Val Ile Ala Thr Lys Asn Gly
595 600 605
Ala Pro Val Glu Ile His Gln Val Leu Asn Asn Gly Leu Leu Val Asp
610 615 620
Pro His Asp Gln Asn Ala Ile Ala Asp Ala Leu Tyr Lys Leu Leu Ser
625 630 635 640
Glu Lys Gln Leu Trp Ser Arg Cys Arg Glu Asn Gly Leu Lys Asn Ile
645 650 655
His Gln Phe Ser Trp Pro Glu His Cys Lys Asn Tyr Leu Ser Arg Ile
660 665 670
Leu Thr Leu Ser Pro Arg Tyr Pro Ala Phe Ala Ser Asn Asp Asp Gln
675 680 685
Ile Lys Ala Pro Ile Lys Gly Arg Lys Tyr Ile Ile Val Ile Ala Val
690 695 700
Asp Ser Ala Ser Lys Lys Asp Leu Ala Phe Ile Ile Arg Asn Ser Ile
705 710 715 720
Glu Ala Thr Arg Thr Glu Thr Ser Ser Gly Ser Thr Gly Phe Val Leu
725 730 735
Ser Thr Ser Leu Thr Ile Ser Glu Ile His Ser Leu Leu Ile Ser Ala
740 745 750
Gly Met Val Pro Thr Asp Phe Asp Ala Phe Ile Cys Asn Ser Gly Ser
755 760 765
Asp Leu Phe Tyr Pro Ser Gln Thr Gly Asp Ser Pro Ser Thr Ser Arg
770 775 780
Val Thr Phe Ala Leu Asp Arg Asn Tyr Gln Ser Arg Val Glu Tyr His
785 790 795 800
Trp Gly Gly Glu Gly Leu Arg Lys Tyr Leu Val Lys Trp Ala Ser Ser
805 810 815
Val Val Glu Arg Arg Gly Arg Met Glu Lys Gln Val Ile Phe Asp Asp
820 825 830

Ser Glu His Ser Ser Thr Cys Cys Leu Ala Phe Arg Val Val Asn Pro
835 840 845
Asn Tyr Leu Pro Pro Leu Lys Glu Leu Gln Lys Leu Met Arg Val Gln
850 855 860
Ser Leu Arg Cys His Ala Leu Tyr Asn His Ser Ala Thr Arg Leu Ser
865 870 875 880
Val Ile Pro Ile His Ala Ser Arg Ser Gln Ala Ile Arg Tyr Leu Ser
885 890 895
Val Arg Trp Gly Ile Glu Leu Pro Asn Val Val Ile Leu Val Gly Glu
900 905 910
Ser Gly Asp Ser Asp Tyr Glu Glu Leu Phe Gly Gly Leu His Lys Thr
915 920 925
Val Val Leu Asn Gly Glu Phe Asn Thr Pro Ala Asn Arg Ile His Thr
930 935 940
Val Arg Arg Tyr Pro Leu Gln Asp Val Ile Ala Leu Asp Cys Ser Asn
945 950 955 960
Ile Val Gly Val Gln Gly Cys Ser Thr Asp Cys Met Arg Ser Thr Leu
965 970 975
Glu Lys Leu Gly Ile Pro Thr Lys
980

<210> 66
<211> 522
<212> PRT
<213> Festuca arundinacea

<400> 66
Met Val Arg Gly Gly Gly Asn Gly Glu Val Glu Leu Ser Val Gly Ala
1 5 10 15
Gly Gly Gly Gly Gly Gly Ala Gly Gly Leu Val Glu Pro Pro Val Pro
20 25 30
Ile Ser Leu Gly Arg Leu Val Leu Ala Gly Met Val Ala Gly Gly Val
35 40 45
Gln Tyr Gly Trp Ala Leu Gln Leu Ser Leu Leu Thr Pro Tyr Val Gln
50 55 60
Thr Leu Gly Leu Ser His Ala Leu Thr Ser Phe Met Trp Leu Cys Gly
65 70 75 80
Pro Ile Ala Gly Leu Val Val Gln Pro Cys Val Gly Leu Tyr Ser Asp
85 90 95
Lys Cys Thr Ser Arg Trp Gly Arg Arg Arg Pro Phe Ile Met Thr Gly
100 105 110
Cys Val Leu Ile Cys Ile Ala Val Val Ile Val Gly Phe Ser Ala Asp
115 120 125
Ile Gly Ala Ala Leu Gly Asp Ser Lys Glu Glu Cys Ser Leu Tyr His
130 135 140
Gly Pro Arg Trp His Ala Ala Ile Val Tyr Val Leu Gly Phe Trp Leu
145 150 155 160
Leu Asp Phe Ser Asn Asn Thr Val Gln Gly Pro Ala Arg Ala Leu Met
165 170 175
Ala Asp Leu Ser Gly Lys Tyr Gly Pro Ser Ala Ala Asn Ser Ile Phe
180 185 190
Cys Ser Trp Met Ala Leu Gly Asn Ile Leu Gly Tyr Ser Ser Gly Ser
195 200 205
Thr Asp Lys Trp His Lys Trp Phe Pro Phe Leu Arg Thr Arg Ala Cys
210 215 220
Cys Glu Ala Cys Ala Asn Leu Lys Gly Ala Phe Leu Val Ala Val Leu
225 230 235 240
Phe Leu Cys Met Cys Leu Val Ile Thr Leu Ile Phe Ala Lys Glu Val
245 250 255
Pro Tyr Lys Arg Ile Ala Pro Leu Pro Thr Lys Ala Asn Gly Gln Val
260 265 270
Glu Val Glu Pro Ser Gly Pro Leu Ala Val Phe Gln Gly Ile Arg Asn
275 280 285
Leu Pro Ser Gly Met Pro Ser Val Leu Leu Val Thr Gly Leu Thr Trp
290 295 300
Leu Ser Trp Phe Pro Phe Ile Leu Tyr Asp Thr Asp Trp Met Gly Arg
305 310 315 320
Glu Ile Tyr His Gly Asp Pro Lys Gly Thr Pro Ala Glu Met Ser Ala

325 330 335
Phe Gln Asp Gly Val Arg Ala Gly Ala Phe Gly Leu Leu Leu Asn Ser
340 345 350
Ile Ile Leu Gly Phe Ser Ser Phe Leu Ile Glu Pro Met Cys Lys Arg
355 360 365
Leu Gly Pro Arg Val Val Trp Val Ser Ser Asn Phe Leu Val Cys Ile
370 375 380
Ala Met Ala Ala Thr Ala Ile Ile Ser Trp Trp Ser Thr Lys Glu Phe
385 390 395 400
His Glu Tyr Val Gln His Ala Ile Thr Ala Ser Lys Asp Ile Lys Ile
405 410 415
Val Cys Met Ala Leu Phe Ala Phe Leu Gly Val Pro Leu Ala Ile Leu
420 425 430
Tyr Ser Val Pro Phe Ala Val Thr Ala Gln Leu Ala Ala Ser Lys Gly
435 440 445
Gly Gly Gln Gly Leu Cys Thr Gly Val Leu Asn Ile Ser Ile Val Ile
450 455 460
Pro Gln Val Ile Ile Ala Leu Gly Ala Gly Pro Trp Asp Gln Leu Phe
465 470 475 480
Gly Lys Gly Asn Ile Pro Ala Phe Ala Ala Ala Ser Ala Phe Ala Leu
485 490 495
Ile Gly Gly Ile Val Gly Ile Phe Leu Leu Pro Lys Ile Ser Arg Arg
500 505 510
Ser Phe Arg Ala Val Ser Thr Gly Gly His
515 520

<210> 67
<211> 407
<212> PRT
<213> Festuca arundinacea

<400> 67
Ile Cys Val Ala Val Val Val Val Gly Phe Ser Ala Asp Ile Gly Ala
1 5 10 15
Ala Leu Gly Asp Ser Lys Glu Glu Cys Ser Leu Tyr His Gly Pro Arg
20 25 30
Trp His Ala Ala Ile Val Tyr Val Leu Gly Phe Trp Leu Leu Asp Phe
35 40 45
Ser Asn Asn Thr Val Gln Gly Pro Ala Arg Ala Leu Met Ala Asp Leu
50 55 60
Ser Gly Lys Tyr Gly Pro Ser Ala Ala Asn Ser Ile Phe Cys Ser Trp
65 70 75 80
Met Ala Leu Gly Asn Ile Leu Gly Tyr Ser Ser Gly Ser Thr Asp Lys
85 90 95
Trp His Lys Trp Phe Pro Phe Leu Arg Thr Arg Ala Cys Cys Glu Ala
100 105 110
Cys Ala Asn Leu Lys Gly Ala Phe Leu Val Ala Val Leu Phe Leu Cys
115 120 125
Phe Cys Leu Val Ile Thr Leu Ile Phe Ala Lys Glu Val Pro Tyr Lys
130 135 140
Arg Ile Ala Pro Leu Pro Thr Lys Ala Asn Gly Gln Val Glu Val Glu
145 150 155 160
Pro Ser Gly Pro Leu Ala Val Phe Gln Gly Phe Arg Asn Leu Pro Ser
165 170 175
Gly Met Pro Ser Val Leu Leu Val Thr Gly Leu Thr Trp Leu Ser Trp
180 185 190
Phe Pro Phe Ile Leu Tyr Asp Thr Asp Trp Met Gly Arg Glu Ile Tyr
195 200 205
His Gly Asp Pro Lys Gly Thr Pro Ala Glu Ala Ser Ala Phe Gln Asp
210 215 220
Gly Val Arg Ala Gly Ala Phe Gly Leu Leu Leu Asn Ser Ile Ile Leu
225 230 235 240
Gly Phe Ser Ser Phe Leu Ile Glu Pro Met Cys Lys Arg Leu Gly Pro
245 250 255
Arg Val Val Trp Val Ser Ser Asn Leu Leu Val Cys Ile Ala Met Ala
260 265 270
Ala Thr Ala Ile Ile Ser Trp Trp Ser Thr Lys Glu Phe His Glu Tyr
275 280 285

Val Gln His Ala Ile Thr Ala Ser Lys Asp Ile Lys Ile Val Cys Met
290 295 300
Val Leu Phe Ala Phe Leu Gly Val Pro Leu Ala Ile Leu Tyr Ser Val
305 310 315 320
Pro Phe Ala Val Thr Ala Gln Leu Ala Ala Asn Lys Gly Gly Gly Gln
325 330 335
Gly Leu Cys Thr Gly Val Leu Asn Ile Ser Ile Val Ile Pro Gln Val
340 345 350
Ile Ile Ala Leu Gly Ala Gly Pro Trp Asp Gln Leu Phe Gly Lys Gly
355 360 365
Asn Ile Pro Ala Phe Ala Ala Ala Ser Ala Phe Ala Leu Ile Gly Gly
370 375 380
Ile Val Gly Ile Phe Leu Leu Pro Lys Ile Ser Arg His Ser Phe Arg
385 390 395 400
Ala Val Ser Thr Gly Gly His
405

<210> 68
<211> 522
<212> PRT
<213> Festuca arundinacea

<400> 68
Met Val Arg Gly Gly Gly Asn Ser Glu Val Glu Leu Ser Val Gly Ala
1 5 10 15
Gly Gly Gly Gly Gly Gly Ala Gly Gly Leu Val Glu Pro Pro Val Pro
20 25 30
Ile Ser Leu Gly Arg Leu Val Phe Ala Gly Met Val Ala Gly Gly Val
35 40 45
Gln Tyr Gly Trp Ala Leu Gln Leu Ser Leu Leu Thr Pro Tyr Val Gln
50 55 60
Thr Leu Gly Leu Ser His Ala Leu Thr Ser Phe Met Trp Leu Cys Gly
65 70 75 80
Pro Ile Ala Gly Leu Val Val Gln Pro Cys Val Gly Leu Tyr Ser Asp
85 90 95
Lys Cys Thr Ser Arg Trp Gly Arg Arg Arg Pro Phe Ile Met Thr Gly
100 105 110
Cys Val Leu Ile Cys Ile Ala Val Val Ile Val Gly Phe Ser Ala Asp
115 120 125
Ile Gly Ala Ala Leu Gly Asp Ser Lys Glu Glu Cys Ser Leu Tyr His
130 135 140
Gly Pro Arg Trp His Ala Ala Ile Val Tyr Val Leu Gly Phe Trp Leu
145 150 155 160
Leu Asp Phe Ser Asn Asn Thr Val Gln Gly Pro Ala Arg Ala Leu Met
165 170 175
Ala Asp Leu Ser Gly Lys Tyr Gly Pro Ser Ala Ala Asn Ser Ile Phe
180 185 190
Cys Ser Trp Met Ala Leu Gly Asn Ile Leu Gly Tyr Ser Ser Gly Ser
195 200 205
Thr Asp Lys Trp His Lys Trp Phe Pro Phe Leu Arg Thr Arg Ala Cys
210 215 220
Cys Glu Ala Cys Ala Asn Leu Lys Gly Ala Phe Leu Val Ala Val Leu
225 230 235 240
Phe Leu Cys Phe Cys Leu Val Ile Thr Leu Ile Phe Ala Lys Glu Val
245 250 255
Pro Tyr Lys Arg Ile Ala Pro Leu Pro Thr Lys Ala Asn Gly Gln Val
260 265 270
Glu Val Glu Pro Ser Gly Pro Leu Ala Val Phe Gln Gly Phe Arg Asn
275 280 285
Leu Pro Ser Gly Met Pro Ser Val Leu Leu Val Thr Gly Leu Thr Trp
290 295 300
Leu Ser Trp Phe Pro Phe Ile Leu Tyr Asp Thr Asp Trp Met Gly Arg
305 310 315 320
Glu Ile Tyr His Gly Asp Pro Lys Gly Thr Pro Ala Glu Ala Ser Ala
325 330 335
Phe Gln Asp Gly Val Arg Ala Gly Ala Phe Gly Leu Leu Leu Asn Ser
340 345 350
Ile Ile Leu Gly Phe Ser Ser Phe Leu Ile Glu Pro Met Cys Lys Arg

```
        355                     360                     365
Leu Gly Pro Arg Val Val Trp Val Ser Ser Asn Leu Leu Val Cys Ile
    370                     375                     380
Ala Met Ala Ala Thr Ala Ile Ile Ser Trp Trp Ser Thr Lys Glu Phe
385                     390                     395                 400
His Glu Tyr Val Gln His Ala Ile Thr Ala Ser Lys Asp Ile Lys Ile
                405                     410                     415
Val Cys Met Val Leu Phe Ala Phe Leu Gly Val Pro Leu Ala Ile Leu
            420                     425                     430
Tyr Ser Val Pro Phe Ala Val Thr Ala Gln Leu Ala Ala Asn Lys Gly
        435                     440                     445
Gly Gly Gln Gly Leu Cys Thr Gly Val Leu Asn Ile Ser Ile Val Ile
    450                     455                     460
Pro Gln Val Ile Ile Ala Leu Gly Ala Gly Pro Trp Asp Gln Leu Phe
465                     470                     475                 480
Gly Lys Gly Asn Ile Pro Ala Phe Ala Ala Ala Ser Ala Phe Ala Leu
                485                     490                     495
Ile Gly Gly Ile Val Gly Ile Phe Leu Leu Pro Lys Ile Ser Arg His
            500                     505                     510
Ser Phe Arg Ala Val Ser Thr Gly Gly His
        515                     520
```

<210> 69
<211> 506
<212> PRT
<213> Lolium perenne

<400> 69

```
Met Pro Pro Pro Arg Arg Pro Thr Thr Gly Gly Thr Thr Thr Thr Ser
1               5                   10                  15
Ala Ala Leu Pro Pro Pro Arg Lys Val Pro Leu Arg Ser Leu Leu Arg
            20                  25                  30
Ala Ala Ser Val Ala Cys Gly Val Gln Phe Gly Trp Ala Leu Gln Leu
        35                  40                  45
Ser Leu Leu Thr Pro Tyr Val Gln Glu Leu Gly Ile Pro His Ala Phe
    50                  55                  60
Ala Ser Leu Val Trp Leu Cys Gly Pro Leu Ser Gly Leu Leu Val Gln
65                  70                  75                  80
Pro Leu Ile Gly His Leu Ser Asp Arg Ile Ala Pro Ala Asp Ser Pro
                85                  90                  95
Leu Gly Arg Arg Arg Pro Phe Ile Ala Ala Gly Ala Ala Ser Ile Ala
            100                 105                 110
Phe Ser Val Leu Thr Val Gly Phe Ser Ala Asp Leu Gly Arg Leu Phe
        115                 120                 125
Gly Asp Asn Val Arg Pro Gly Ser Thr Arg Tyr Gly Ala Ile Ile Val
    130                 135                 140
Tyr Met Ile Gly Phe Trp Leu Leu Asp Val Gly Asn Asn Ala Thr Gln
145                 150                 155                 160
Gly Pro Cys Arg Ala Phe Leu Ala Asp Leu Thr Glu Asn Asp Pro Arg
                165                 170                 175
Arg Thr Arg Ile Ala Asn Ala Tyr Phe Ser Leu Phe Met Ala Leu Gly
            180                 185                 190
Asn Ile Leu Gly Tyr Ala Thr Gly Ala Tyr Ser Gly Trp Tyr Lys Ile
        195                 200                 205
Phe Pro Phe Thr Ile Thr Glu Ser Cys Gly Val Ser Cys Ala Asn Leu
    210                 215                 220
Lys Ser Ala Phe Leu Leu Asp Ile Ile Ile Leu Ala Ile Thr Thr Tyr
225                 230                 235                 240
Val Thr Val Val Thr Val Gln Asp Asn Pro Thr Phe Gly Ser Asp Glu
                245                 250                 255
Ala Ala Pro Arg Pro Ser Ser His Glu Glu Glu Ala Phe Leu Phe Glu
            260                 265                 270
Leu Phe Gly Ser Phe Lys Tyr Phe Thr Met Pro Val Trp Met Val Leu
        275                 280                 285
Ile Val Thr Ser Leu Thr Trp Ile Gly Trp Phe Pro Phe Ile Leu Phe
    290                 295                 300
Asp Thr Asp Trp Met Gly Arg Glu Ile Tyr Arg Gly Ser Pro Glu Ile
305                 310                 315                 320
```

```
Val Ala Asp Thr Gln Lys Tyr His Asp Gly Val Arg Met Gly Ser Phe
                325                 330                 335
Gly Leu Met Leu Asn Ser Val Leu Leu Gly Ile Thr Ser Val Val Thr
            340                 345                 350
Glu Lys Leu Cys Arg Lys Trp Gly Ala Gly Leu Val Trp Gly Val Ser
        355                 360                 365
Asn Ile Ile Met Ala Leu Cys Phe Val Ala Met Leu Val Ile Thr Tyr
    370                 375                 380
Val Ala Gln Asn Leu Asp Tyr Gly Pro Ser Gly Ala Pro Pro Thr Gly
385                 390                 395                 400
Ile Val Val Ala Ser Leu Thr Val Phe Thr Ile Leu Gly Ala Pro Leu
                405                 410                 415
Ser Ile Thr Tyr Ser Ile Pro Tyr Ala Met Ala Thr Ser Arg Val Glu
            420                 425                 430
Asn Leu Gly Leu Gly Gln Gly Leu Ala Met Gly Ile Leu Asn Leu Ser
        435                 440                 445
Ile Val Ile Pro Gln Ile Ile Val Ser Leu Gly Ser Gly Pro Trp Asp
    450                 455                 460
Ser Leu Phe Gly Gly Gly Asn Ala Pro Ser Phe Trp Val Ala Ala Ala
465                 470                 475                 480
Ala Ser Phe Ile Gly Gly Leu Val Ala Ile Leu Gly Leu Pro Arg Ala
                485                 490                 495
Arg Ile Ala Pro Lys Lys Arg Ser Gln Arg
            500                 505
```

<210> 70
<211> 504
<212> PRT
<213> Festuca arundinacea

<400> 70

```
Met Pro Pro Pro Arg Arg Pro Asn Ala Gly Gly Thr Thr Ser Ala Pro
1               5                   10                  15
Leu Pro Pro Pro Arg Lys Val Pro Leu Arg Ser Leu Leu Arg Ala Ala
            20                  25                  30
Ser Val Ala Cys Gly Val Gln Phe Gly Trp Ala Leu Gln Leu Ser Leu
        35                  40                  45
Leu Thr Pro Tyr Val Gln Glu Leu Gly Ile Pro His Ala Phe Ala Ser
    50                  55                  60
Leu Val Trp Leu Cys Gly Pro Leu Ser Gly Leu Leu Val Gln Pro Leu
65                  70                  75                  80
Ile Gly His Leu Ser Asp Arg Ile Ala Pro Ala Asp Ser Pro Leu Gly
                85                  90                  95
Arg Arg Arg Pro Phe Ile Ala Ala Gly Ala Ala Ser Ile Ala Phe Ser
            100                 105                 110
Val Leu Thr Val Gly Phe Ser Ala Asp Leu Gly Arg Leu Phe Gly Asp
        115                 120                 125
Asn Ile Arg Pro Gly Ser Thr Arg Phe Gly Ala Ile Ile Val Tyr Met
    130                 135                 140
Ile Gly Phe Trp Leu Leu Asp Val Gly Asn Asn Ala Thr Gln Gly Pro
145                 150                 155                 160
Cys Arg Ala Phe Leu Ala Asp Leu Thr Glu Asn Asp Pro Arg Arg Thr
                165                 170                 175
Arg Ile Ala Asn Ala Tyr Phe Ser Leu Phe Met Ala Leu Gly Asn Ile
            180                 185                 190
Leu Gly Tyr Ala Thr Gly Ala Tyr Ser Gly Trp Tyr Lys Ile Phe Pro
        195                 200                 205
Phe Thr Ile Thr Glu Ser Cys Gly Val Ser Cys Ala Asn Leu Lys Ser
    210                 215                 220
Ala Phe Leu Leu Asp Ile Ile Ile Leu Ala Ile Thr Thr Tyr Val Thr
225                 230                 235                 240
Val Val Thr Val Gln Asp Asn Pro Thr Phe Gly Ser Asp Glu Ala Ala
                245                 250                 255
Pro Arg Pro Ser Ser His Glu Glu Glu Ala Phe Leu Phe Glu Leu Phe
            260                 265                 270
Gly Ser Phe Lys Tyr Phe Thr Leu Pro Val Trp Met Val Leu Ile Val
        275                 280                 285
Thr Ser Leu Thr Trp Ile Gly Trp Phe Pro Phe Ile Leu Phe Asp Thr
```

```
    290                     295                     300
Asp Trp Met Gly Arg Glu Ile Tyr Arg Gly Ser Pro Glu Ile Val Ala
305                     310                     315                 320
Asp Thr Gln Lys Tyr His Asp Gly Val Arg Met Gly Ser Phe Gly Leu
                325                     330                     335
Met Leu Asn Ser Val Leu Leu Gly Ile Thr Ser Val Val Met Glu Lys
            340                     345                     350
Leu Cys Arg Lys Trp Gly Ala Gly Leu Val Trp Gly Val Ser Asn Ile
        355                     360                     365
Ile Met Ala Leu Cys Phe Val Ala Met Leu Ile Ile Thr Tyr Val Ala
    370                     375                     380
Lys Asn Leu Asp Tyr Gly Pro Ser Gly Ala Pro Pro Thr Gly Ile Val
385                     390                     395                 400
Val Ala Ser Leu Ala Val Phe Thr Ile Leu Gly Ala Pro Leu Ser Ile
                405                     410                     415
Thr Tyr Ser Ile Pro Tyr Ala Met Ala Thr Ser Arg Val Glu Asn Leu
            420                     425                     430
Gly Leu Gly Gln Gly Leu Ala Met Gly Ile Leu Asn Leu Ser Ile Val
        435                     440                     445
Ile Pro Gln Ile Ile Val Ser Leu Gly Ser Gly Pro Trp Asp Ser Leu
    450                     455                     460
Phe Gly Gly Gly Asn Ala Pro Ser Phe Trp Val Ala Ala Ala Ala Ser
465                     470                     475                 480
Phe Ile Gly Gly Leu Val Ala Ile Leu Gly Leu Pro Arg Ala Arg Ile
                485                     490                     495
Ala Pro Lys Lys Arg Ser Gln Arg
            500

&lt;210&gt; 71
&lt;211&gt; 508
&lt;212&gt; PRT
&lt;213&gt; Lolium perenne

&lt;400&gt; 71
Met Val Asp Gln Asp His Asp Gly Arg Arg Arg Gln Glu Glu Ala Thr
 1               5                  10                  15
Ala Val Ala Ala Ser Ser Val Pro Leu Leu Glu Lys Lys Pro Gly Asp
            20                  25                  30
Val Pro Tyr Tyr Val Glu Gly Cys Pro Gly Cys Ala Val Asp Arg Arg
        35                  40                  45
Lys Ala Thr Asp Pro Gly Ile Pro Tyr Gly Ser Phe Ile Tyr Ile Trp
    50                  55                  60
Val Val Ile Leu Cys Thr Ala Ile Pro Ile Ser Ser Leu Phe Pro Phe
65                  70                  75                  80
Leu Tyr Phe Met Ile Arg Asp Leu His Ile Ala Glu Arg Thr Glu Asp
                85                  90                  95
Ile Gly Phe Tyr Ala Gly Phe Val Gly Ala Ala Phe Met Phe Gly Arg
            100                 105                 110
Cys Leu Thr Ser Thr Ile Trp Gly Ile Ala Ala Asp Arg Ile Gly Arg
        115                 120                 125
Lys Pro Val Val Ile Phe Gly Val Phe Ser Val Val Ile Phe Asn Ala
    130                 135                 140
Leu Phe Gly Leu Ser Val Thr Tyr Trp Met Ala Ile Ala Thr Arg Phe
145                 150                 155                 160
Leu Leu Gly Ala Leu Asn Gly Leu Leu Gly Pro Met Lys Ala Tyr Ala
                165                 170                 175
Ile Glu Val Cys Arg Pro Glu His Glu Ala Leu Ala Leu Ser Leu Val
            180                 185                 190
Ser Thr Ala Trp Gly Ile Gly Leu Ile Ile Gly Pro Ala Leu Gly Gly
        195                 200                 205
Tyr Leu Ala Leu Pro Ala Glu Lys Tyr Pro Asn Ile Phe Ser Pro Asp
    210                 215                 220
Ser Leu Phe Gly Arg Phe Pro Tyr Phe Leu Pro Cys Leu Cys Thr Ser
225                 230                 235                 240
Val Phe Ala Ala Ala Val Leu Ile Gly Cys Ile Trp Met Pro Glu Thr
                245                 250                 255
Leu His Lys His Lys Val Asn Glu Asn Arg Asn Gln Ser Val Glu Ser
            260                 265                 270
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Leu Glu Ala His Leu Ile Asp Pro Lys Glu Lys Val Glu Gln Ser Asn
275 280 285
Ser Pro Asp Thr Lys Lys Ser Leu Phe Lys Asn Trp Pro Leu Met Ser
290 295 300
Ser Ile Ile Val Tyr Cys Val Phe Ser Phe His Asp Met Ala Tyr Thr
305 310 315 320
Glu Val Phe Ser Leu Trp Ala Glu Ser Asp Arg Thr Tyr Gly Gly Leu
325 330 335
Ser Leu Ser Ser Glu Asp Val Gly Gln Thr Leu Ala Ile Thr Gly Ser
340 345 350
Ser Leu Leu Val Tyr Gln Leu Phe Leu Tyr Pro Arg Ile Asn Arg Val
355 360 365
Leu Gly Pro Ile Lys Ser Ser Gln Ile Ala Ala Gly Ile Cys Ile Pro
370 375 380
Ile Leu Phe Ala Tyr Pro Tyr Met Thr Tyr Leu Ser Glu Pro Gly Leu
385 390 395 400
Ser Ile Val Leu Asn Ile Ala Ser Val Ile Lys Asn Asn Leu Gly Val
405 410 415
Thr Ile Ile Thr Gly Thr Phe Ile Leu Gln Asn Asn Ala Val Pro Gln
420 425 430
Asp Gln Arg Gly Ala Ala Asn Gly Leu Ala Met Thr Gly Met Ser Phe
435 440 445
Phe Lys Ala Val Ala Pro Ala Gly Ala Gly Ile Val Phe Ser Trp Ala
450 455 460
Gln Lys Arg Gln His Ala Phe Phe Phe Pro Gly Asp Gln Met Val Phe
465 470 475 480
Phe Leu Leu Asn Ile Ile Glu Leu Leu Gly Leu Leu Leu Thr Phe Lys
485 490 495
Phe Phe Leu Ala Val Pro Asp Lys Ser Asp Ser Asn
500 505

<210> 72
<211> 522
<212> PRT
<213> Lolium perenne

<400> 72
Met Ser Ser Met Gln Phe Ser Ser Val Leu Pro Leu Glu Gly Lys Ala
1 5 10 15
Cys Val Cys Pro Val Arg Ser Ala Asn Asn Gly Cys Glu Arg Leu Lys
20 25 30
Val Gly Asp Ser Ser Ser Leu Arg His Glu Met Ala Leu Arg Arg Lys
35 40 45
Cys Asn Gly Ala Arg Gly Gly Gly Ala Ala Asn Gly Ala Gln Cys Val
50 55 60
Leu Thr Ser Asp Ala Ser Pro Asp Thr Leu Val Val Arg Ser Ser Phe
65 70 75 80
Arg Arg Asn Tyr Ala Asp Pro Asn Glu Val Ala Ala Val Ile Leu Gly
85 90 95
Gly Gly Thr Gly Thr Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr
100 105 110
Pro Ala Val Pro Ile Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met
115 120 125
Ser Asn Cys Phe Asn Ser Gly Ile Asn Lys Ile Phe Val Met Thr Gln
130 135 140
Phe Asn Ser Ala Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Gly
145 150 155 160
Gly Gly Ile Asn Phe Thr Asp Gly Ser Val Glu Val Leu Ala Ala Thr
165 170 175
Gln Met Pro Gly Glu Ala Ala Gly Trp Phe Arg Gly Thr Ala Asp Ala
180 185 190
Val Arg Lys Phe Ile Trp Val Leu Glu Asp Tyr Tyr Lys His Lys Ser
195 200 205
Ile Glu His Ile Leu Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asp
210 215 220
Tyr Met Glu Leu Val Gln Lys His Val Asp Asp Asn Ala Asp Ile Thr
225 230 235 240
Leu Ser Cys Ala Pro Val Gly Glu Ser Arg Ala Ser Glu Tyr Gly Leu

245 250 255
Val Lys Phe Asp Ser Ser Gly Arg Val Ile Gln Phe Ser Glu Lys Pro
260 265 270
Lys Gly Ala Asp Leu Glu Ala Met Lys Val Asp Thr Ser Phe Leu Asn
275 280 285
Phe Ala Ile Asp Asp Pro Ala Lys Asn Pro Tyr Ile Ala Ser Met Gly
290 295 300
Val Tyr Val Phe Lys Arg Glu Val Leu Leu Asn Leu Leu Lys Ser Arg
305 310 315 320
Tyr Thr Glu Leu His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Leu
325 330 335
His Asp His Asn Val Gln Ala Tyr Val Phe Thr Asp Tyr Trp Glu Asp
340 345 350
Ile Gly Thr Ile Arg Ser Phe Phe Asp Ala Asn Met Ala Leu Cys Glu
355 360 365
Gln Pro Pro Lys Phe Glu Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr
370 375 380
Ser Pro Arg Tyr Leu Pro Pro Thr Lys Ser Asp Lys Cys Arg Ile Lys
385 390 395 400
Glu Ala Ile Ile Ser His Gly Cys Phe Leu Arg Glu Cys Thr Ile Glu
405 410 415
His Ser Ile Ile Gly Val Arg Ser Arg Leu Asn Ser Gly Ser Val Leu
420 425 430
Lys Asn Ala Met Met Met Gly Ala Asp Leu Tyr Glu Thr Glu Asp Glu
435 440 445
Ile Ser Gly Leu Leu Ser Glu Gly Lys Val Pro Ile Gly Val Gly Glu
450 455 460
Asn Ser Lys Leu Ser Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly
465 470 475 480
Arg Asp Val Val Ile Ala Asn Ser Glu Gly Val Gln Glu Ala Asp Arg
485 490 495
Pro Glu Glu Gly Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys
500 505 510
Asn Ala Thr Val Lys Asp Gly Thr Val Val
515 520

<210> 73
<211> 522
<212> PRT
<213> Festuca arundinacea

<400> 73
Met Ser Ser Met Gln Phe Ser Ser Val Leu Pro Leu Glu Gly Lys Ala
1 5 10 15
Cys Val Cys Pro Val Arg Ser Ala Asn Asn Gly Cys Glu Arg Leu Lys
20 25 30
Val Gly Asp Ser Ser Ser Leu Arg His Glu Met Ala Leu Arg Arg Lys
35 40 45
Cys Asn Gly Ala Arg Gly Gly Gly Ala Ala Asp Gly Ala Gln Cys Val
50 55 60
Leu Thr Ser Asp Ala Ser Pro Asp Thr Leu Val Val Arg Ser Ser Phe
65 70 75 80
Arg Met Asn Tyr Ala Asp Pro Asn Glu Val Ala Ala Val Ile Leu Gly
85 90 95
Gly Gly Thr Gly Thr Gln Leu Phe Pro Leu Thr Ser Thr Arg Ala Thr
100 105 110
Pro Ala Val Pro Ile Gly Gly Cys Tyr Arg Leu Ile Asp Ile Pro Met
115 120 125
Ser Asn Cys Phe Asn Ser Gly Ile Asn Lys Ile Phe Val Met Thr Gln
130 135 140
Phe Asn Ser Ala Ser Leu Asn Arg His Ile His Arg Thr Tyr Leu Gly
145 150 155 160
Gly Gly Ile Asn Phe Thr Asp Gly Ser Val Glu Val Leu Ala Ala Thr
165 170 175
Gln Met Pro Gly Glu Ala Ala Gly Trp Phe Arg Gly Thr Ala Asp Ala
180 185 190
Val Arg Lys Phe Ile Trp Val Leu Glu Asp Tyr Tyr Lys His Lys Ser
195 200 205

Ile Glu His Ile Leu Ile Leu Ser Gly Asp Gln Leu Tyr Arg Met Asp
210 215 220
Tyr Met Glu Leu Val Gln Lys His Val Asp Asp Asn Ala Asp Ile Thr
225 230 235 240
Leu Ser Cys Ala Pro Val Gly Glu Ser Arg Ala Ser Glu Tyr Gly Leu
245 250 255
Val Lys Phe Asp Ser Ser Gly Arg Val Ile Gln Phe Ser Glu Lys Pro
260 265 270
Lys Gly Ala Asp Leu Glu Ala Met Lys Val Asp Thr Ser Phe Leu Asn
275 280 285
Phe Ala Ile Asp Asp Pro Ala Lys Asn Pro Tyr Ile Ala Ser Met Gly
290 295 300
Val Tyr Val Phe Lys Arg Glu Val Leu Leu Asn Leu Leu Lys Ser Arg
305 310 315 320
Tyr Thr Glu Leu His Asp Phe Gly Ser Glu Ile Leu Pro Arg Ala Leu
325 330 335
His Asp His Asn Val Gln Ala Tyr Val Phe Thr Asp Tyr Trp Glu Asp
340 345 350
Ile Gly Thr Ile Arg Ser Phe Phe Asp Ala Asn Met Ala Leu Cys Glu
355 360 365
Gln Pro Pro Lys Phe Glu Phe Tyr Asp Pro Lys Thr Pro Phe Phe Thr
370 375 380
Ser Pro Arg Tyr Leu Pro Pro Thr Lys Ser Asp Lys Cys Arg Ile Lys
385 390 395 400
Glu Ala Ile Ile Ser His Gly Cys Phe Leu Arg Glu Cys Thr Ile Glu
405 410 415
His Ser Ile Ile Gly Val Arg Ser Arg Leu Asn Ser Gly Ser Val Leu
420 425 430
Lys Asn Ala Met Met Met Gly Ala Asp Leu Tyr Glu Thr Glu Asp Glu
435 440 445
Ile Ser Gly Leu Leu Ser Glu Gly Lys Val Pro Ile Gly Val Gly Glu
450 455 460
Asn Ser Lys Leu Ser Asn Cys Ile Ile Asp Met Asn Ala Arg Ile Gly
465 470 475 480
Arg Asp Val Val Ile Ala Asn Ser Glu Gly Val Gln Glu Ala Asp Arg
485 490 495
Pro Glu Glu Gly Tyr Tyr Ile Arg Ser Gly Ile Val Val Ile Leu Lys
500 505 510
Asn Ala Thr Val Lys Asp Gly Thr Val Val
515 520

<210> 74
<211> 525
<212> PRT
<213> Lolium perenne

<400> 74
Met Thr Gly Ala Pro Pro Ser Thr Val Met Ala Met Gly Ala Ala Thr
1 5 10 15
Ser Pro Cys Lys Ile Leu Ser Ala Thr Gln Arg Ala Ser Thr Ala Ala
20 25 30
Ala Ser Ala Ser Thr Ser Arg Glu Ser Val Ser Leu Arg Ala Pro Arg
35 40 45
Gly Arg Arg Gln Arg Pro Arg Pro Arg Gly Leu Ala Leu Ser Leu Ala
50 55 60
Pro Ala Arg Arg Pro Phe Val Phe Ser Pro Arg Ala Val Ser Asp Ser
65 70 75 80
Lys Ser Ser Gln Thr Cys Leu Asp Pro Asp Ala Ser Thr Ser Val Leu
85 90 95
Gly Ile Ile Leu Gly Gly Gly Ala Gly Thr Arg Leu Tyr Pro Leu Thr
100 105 110
Lys Lys Arg Ala Lys Pro Ala Val Pro Leu Gly Ala Asn Tyr Arg Leu
115 120 125
Ile Asp Ile Pro Val Ser Asn Cys Leu Asn Ser Asn Ile Ser Lys Ile
130 135 140
Tyr Val Leu Thr Gln Phe Asn Ser Ala Ser Leu Asn Arg His Leu Ser
145 150 155 160
Arg Ala Tyr Gly Ser Asn Ile Gly Gly Tyr Lys Asn Glu Gly Phe Val

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                    165                     170                     175
Glu Val Leu Ala Ala Gln Gln Ser Pro Asp Asn Pro Asn Trp Phe Gln
                180                 185                 190
Gly Thr Ala Asp Ala Val Arg Gln Tyr Leu Trp Leu Phe Glu Glu His
            195                 200                 205
Asn Val Met Glu Tyr Leu Ile Leu Ala Gly Asp His Leu Tyr Arg Met
    210                 215                 220
Asp Tyr Glu Lys Phe Ile Gln Ala His Arg Glu Thr Asp Ala Asp Ile
225                 230                 235                 240
Thr Val Ala Ala Leu Pro Met Asp Glu Glu Arg Ala Thr Ala Phe Gly
                245                 250                 255
Leu Met Lys Ile Asp Glu Glu Gly Arg Ile Val Glu Phe Ala Glu Lys
            260                 265                 270
Pro Lys Gly Glu Gln Leu Lys Ala Met Met Val Asp Thr Thr Ile Leu
        275                 280                 285
Gly Leu Asp Asp Val Arg Ala Lys Glu Met Pro Tyr Ile Ala Ser Met
    290                 295                 300
Gly Ile Tyr Val Ile Ser Lys His Val Met Leu Gln Leu Leu Arg Asp
305                 310                 315                 320
Gln Phe Pro Gly Ala Asn Asp Phe Gly Ser Glu Val Ile Pro Gly Ala
                325                 330                 335
Thr Ser Thr Gly Met Arg Val Gln Ala Tyr Leu Tyr Asp Gly Tyr Trp
            340                 345                 350
Glu Asp Ile Gly Thr Ile Glu Ala Phe Tyr Asn Ala Asn Leu Gly Ile
        355                 360                 365
Thr Lys Lys Pro Ile Pro Asp Phe Ser Phe Tyr Asp Arg Ser Ala Pro
    370                 375                 380
Ile Tyr Thr Gln Pro Arg His Leu Pro Pro Ser Lys Val Leu Asp Ala
385                 390                 395                 400
Asp Val Thr Asp Ser Val Ile Gly Glu Gly Cys Val Ile Lys Asn Cys
                405                 410                 415
Lys Ile His His Ser Val Val Gly Leu Arg Ser Cys Ile Ser Glu Gly
            420                 425                 430
Ala Ile Ile Glu Asp Thr Leu Leu Met Gly Ala Asp Tyr Tyr Glu Thr
        435                 440                 445
Glu Ala Asp Lys Lys Leu Leu Ala Asp Lys Gly Gly Ile Pro Ile Gly
    450                 455                 460
Ile Gly Lys Asn Ser His Ile Arg Arg Ala Ile Ile Asp Lys Asn Ala
465                 470                 475                 480
Arg Ile Gly Asp Asn Val Lys Ile Ile Asn Val Asp Asn Val Gln Glu
                485                 490                 495
Ala Ala Arg Glu Thr Asp Gly Tyr Phe Ile Lys Ser Gly Ile Val Thr
            500                 505                 510
Val Ile Lys Asp Ala Leu Leu Pro Ser Gly Thr Val Ile
        515                 520                 525
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<210> 75
<211> 524
<212> PRT
<213> Festuca arundinacea

<400> 75
Met Thr Arg Ala Pro Pro Ser Thr Val Met Ala Met Gly Ala Ala Thr
 1               5                  10                  15
Ser Pro Cys Lys Ile Leu Ser Ala Thr Gln Arg Ala Ser Ala Ala Ala
            20                  25                  30
Pro Ser Ala Ser Thr Ser Arg Glu Ser Val Cys Leu Leu Arg Ala Pro
        35                  40                  45
Arg Gly Arg Arg Gln Arg Pro Arg Gly Leu Ala Leu Ser Leu Ala Pro
    50                  55                  60
Ala Arg Arg Pro Phe Val Phe Ser Pro Arg Ala Val Ser Asp Ser Lys
65                  70                  75                  80
Ser Ser Gln Thr Cys Leu Asp Pro Asp Ala Ser Thr Ser Val Leu Gly
                85                  90                  95
Ile Ile Leu Gly Gly Gly Ala Gly Thr Arg Leu Tyr Pro Leu Thr Lys
            100                 105                 110
Lys Arg Ala Lys Pro Ala Val Pro Leu Gly Ala Asn Tyr Arg Leu Ile
        115                 120                 125
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Asp Ile Pro Val Ser Asn Cys Leu Asn Ser Asn Ile Ser Lys Ile Tyr
    130   135   140
Val Leu Thr Gln Phe Asn Ser Ala Ser Leu Asn Arg His Leu Ser Arg
145   150   155   160
Ala Tyr Gly Ser Asn Ile Gly Gly Tyr Lys Asn Glu Gly Phe Val Glu
                165   170   175
Val Leu Ala Ala Gln Gln Ser Pro Asp Asn Pro Asn Trp Phe Gln Gly
            180   185   190
Thr Ala Asp Ala Val Arg Gln Tyr Leu Trp Leu Phe Glu Glu His Asn
        195   200   205
Val Met Glu Tyr Leu Ile Leu Ala Gly Asp His Leu Tyr Arg Met Asp
    210   215   220
Tyr Glu Lys Phe Ile Gln Ala His Arg Glu Thr Asp Ala Asp Ile Thr
225   230   235   240
Val Ala Ala Leu Pro Met Asp Glu Glu Arg Ala Thr Ala Phe Gly Leu
                245   250   255
Met Lys Ile Asp Glu Glu Gly Arg Ile Val Glu Phe Ala Glu Lys Pro
            260   265   270
Lys Gly Glu Gln Leu Lys Ala Met Met Val Asp Thr Thr Ile Leu Gly
        275   280   285
Leu Asp Asp Val Arg Ala Lys Glu Met Pro Tyr Ile Ala Ser Met Gly
    290   295   300
Ile Tyr Val Ile Ser Lys His Val Met Leu Gln Leu Leu Arg Asp Gln
305   310   315   320
Phe Pro Gly Ala Asn Asp Phe Gly Ser Glu Val Ile Pro Gly Ala Thr
                325   330   335
Ser Thr Gly Met Arg Val Gln Ala Tyr Leu Tyr Asp Gly Tyr Trp Glu
            340   345   350
Asp Ile Gly Thr Ile Glu Ala Phe Tyr Asn Ala Asn Leu Gly Ile Thr
        355   360   365
Lys Lys Pro Ile Pro Asp Phe Ser Phe Tyr Asp Arg Ser Ala Pro Ile
    370   375   380
Tyr Thr Gln Pro Arg His Leu Pro Pro Ser Lys Val Leu Asp Ala Asp
385   390   395   400
Val Thr Asp Ser Val Ile Gly Glu Gly Cys Val Ile Lys Asn Cys Lys
                405   410   415
Ile His His Ser Val Val Gly Leu Arg Ser Cys Ile Ser Glu Gly Ala
            420   425   430
Ile Ile Glu Asp Thr Leu Leu Met Gly Ala Asp Tyr Tyr Glu Thr Glu
        435   440   445
Ala Asp Lys Lys Leu Leu Ala Asp Lys Gly Gly Ile Pro Ile Gly Ile
    450   455   460
Gly Lys Asn Ser His Ile Arg Arg Ala Ile Ile Asp Lys Asn Ala Arg
465   470   475   480
Ile Gly Asp Asn Val Lys Ile Ile Asn Val Asp Asn Val Gln Glu Ala
                485   490   495
Ala Arg Glu Thr Asp Gly Tyr Phe Ile Lys Ser Gly Ile Val Thr Val
            500   505   510
Ile Lys Asp Ala Leu Leu Pro Ser Gly Thr Val Ile
        515   520

<210> 76
<211> 398
<212> PRT
<213> Festuca arundinacea

<400> 76
Met Ala Ala Thr Met Thr Val Glu Glu Val Arg Lys Ala Gln Arg Ala
1   5   10   15
Glu Gly Pro Ala Thr Val Leu Ala Ile Gly Thr Ala Thr Pro Ala Asn
            20   25   30
Cys Val Tyr Gln Ala Asp Tyr Pro Asp Tyr Tyr Phe Lys Ile Thr Lys
        35   40   45
Ser Asp His Leu Ala Asp Leu Lys Glu Lys Phe Lys Arg Met Cys Asp
    50   55   60
Lys Ser Gln Ile Arg Lys Arg Tyr Met His Leu Thr Glu Glu Ile Leu
65   70   75   80
Glu Glu Asn Pro Asn Met Cys Ala Tyr Met Ala Pro Ser Leu Asp Ala

85 90 95
Arg Gln Asp Ile Val Val Val Glu Val Pro Lys Leu Gly Lys Ala Ala
100 105 110
Ala Gln Lys Ala Ile Lys Glu Trp Gly Gln Pro Arg Ser Lys Ile Thr
115 120 125
His Leu Val Phe Cys Thr Thr Ser Gly Val Asp Met Pro Gly Ala Asp
130 135 140
Tyr Gln Leu Thr Lys Met Leu Gly Leu Arg Pro Ser Val Lys Arg Leu
145 150 155 160
Met Met Tyr Gln Gln Gly Cys Phe Ala Gly Gly Thr Val Leu Arg Leu
165 170 175
Ala Lys Asp Leu Ala Glu Asn Asn Arg Gly Ala Arg Val Leu Val Val
180 185 190
Cys Ser Glu Ile Thr Ala Val Thr Phe Arg Gly Pro His Glu Ser His
195 200 205
Leu Asp Ser Leu Val Gly Gln Ala Leu Phe Gly Asp Gly Ala Ala Ala
210 215 220
Val Ile Ile Gly Ala Asp Pro Asp Val Ser Val Glu Arg Pro Leu Phe
225 230 235 240
Gln Leu Val Ser Val Ser Gln Thr Ile Leu Pro Asp Ser Glu Gly Ala
245 250 255
Ile Asp Gly His Leu Arg Glu Val Gly Leu Thr Phe His Leu Leu Lys
260 265 270
Asp Val Pro Gly Leu Ile Ser Lys Asn Ile Glu Arg Ala Leu Glu Glu
275 280 285
Ala Phe Lys Pro Leu Gly Ile Asp Asp Trp Asn Ser Val Phe Trp Val
290 295 300
Ala His Pro Gly Gly Pro Ala Ile Leu Asp Met Val Glu Ala Lys Val
305 310 315 320
Asn Leu Asn Lys Glu Arg Met Arg Ala Thr Arg His Val Leu Ser Glu
325 330 335
Tyr Gly Asn Met Ser Ser Ala Cys Val Leu Phe Ile Met Asp Glu Met
340 345 350
Arg Lys Arg Ser Ala Glu Asp Gly His Thr Thr Thr Gly Glu Gly Met
355 360 365
Asp Trp Gly Val Leu Phe Gly Phe Gly Pro Gly Leu Thr Val Glu Thr
370 375 380
Val Val Leu His Ser Met Pro Ile Ala Ala Asp Ala Thr Ala
385 390 395

<210> 77
<211> 398
<212> PRT
<213> Festuca arundinacea

<400> 77
Met Ala Thr Thr Met Thr Val Glu Glu Val Arg Lys Ala Gln Arg Ala
1 5 10 15
Glu Gly Pro Ala Thr Val Leu Ala Ile Gly Thr Ala Thr Pro Ala Asn
20 25 30
Cys Val Tyr Gln Ala Asp Tyr Pro Asp Tyr Tyr Phe Lys Ile Thr Lys
35 40 45
Ser Asp His Leu Ala Asp Leu Lys Glu Lys Phe Lys Arg Met Cys Asp
50 55 60
Lys Ser Gln Ile Arg Lys Arg Tyr Met His Leu Thr Glu Glu Ile Leu
65 70 75 80
Glu Glu Asn Pro Asn Met Cys Ala Tyr Met Ala Pro Ser Leu Asp Ala
85 90 95
Arg Gln Asp Ile Val Val Val Glu Val Pro Lys Leu Gly Lys Ala Ala
100 105 110
Ala Gln Lys Ala Ile Lys Glu Trp Gly Gln Pro Arg Ser Lys Ile Thr
115 120 125
His Leu Val Phe Cys Thr Thr Ser Gly Val Asp Met Pro Gly Ala Asp
130 135 140
Tyr Gln Leu Thr Lys Met Leu Gly Leu Arg Pro Ser Val Lys Arg Leu
145 150 155 160
Met Met Tyr Gln Gln Gly Cys Phe Ala Gly Gly Thr Val Leu Arg Leu
165 170 175

Ala Lys Asp Leu Ala Glu Asn Asn Arg Gly Ala Arg Val Leu Val Val
180 185 190
Cys Ser Glu Ile Thr Ala Val Thr Phe Arg Gly Pro His Glu Ser His
195 200 205
Leu Asp Ser Leu Val Gly Gln Ala Leu Phe Gly Asp Gly Ala Ala Ala
210 215 220
Val Ile Ile Gly Ala Asp Pro Asp Val Ser Val Glu His Pro Leu Phe
225 230 235 240
Gln Leu Val Ser Ala Ser Gln Thr Ile Leu Pro Asp Ser Glu Gly Ala
245 250 255
Ile Asp Gly His Leu Arg Glu Val Gly Leu Thr Phe His Leu Leu Lys
260 265 270
Asp Val Pro Gly Leu Ile Ser Lys Asn Ile Glu Arg Ala Leu Glu Glu
275 280 285
Ala Phe Lys Pro Leu Gly Ile Asp Asp Trp Asn Ser Val Phe Trp Val
290 295 300
Ala His Pro Gly Gly Pro Ala Ile Leu Asp Met Val Glu Ala Lys Val
305 310 315 320
Asn Leu Asn Lys Glu Arg Met Arg Ala Thr Arg His Val Leu Ser Glu
325 330 335
Tyr Gly Asn Met Ser Ser Ala Cys Val Leu Phe Ile Met Asp Glu Met
340 345 350
Arg Lys Arg Ser Ala Glu Asp Gly His Thr Thr Thr Gly Glu Gly Met
355 360 365
Asp Trp Gly Val Leu Phe Gly Phe Gly Pro Gly Leu Thr Val Glu Thr
370 375 380
Val Val Leu His Ser Met Pro Ile Ala Ala Gly Ala Thr Ala
385 390 395

<210> 78
<211> 277
<212> PRT
<213> Festuca arundinacea

<400> 78
Arg Ala Asp Leu Glu Glu Glu Gly Ser Phe Asp Asp Ala Val Ala Gly
1 5 10 15
Cys Asp Tyr Ala Phe Leu Val Ala Ala Pro Val Asn Leu Lys Ala Glu
20 25 30
Asn Pro Glu Lys Asp Met Val Glu Pro Ala Val Gly Gly Thr Leu Asn
35 40 45
Ala Met Arg Ser Cys Val Arg Ala Gly Thr Val Lys Arg Val Val Leu
50 55 60
Thr Ser Ser Val Ala Ser Val Ser Ala Arg Pro Leu Leu Gln Gly Asp
65 70 75 80
Gly His Val Leu Asp Glu Glu Ser Trp Ser Asp Val Asp Phe Leu Arg
85 90 95
Ala Lys Ala Thr Gly His Trp Gly Tyr Pro Val Ser Lys Val Leu Leu
100 105 110
Glu Lys Ala Ala Cys Ala Phe Ala Gln Ala Ser Gly Ile Ser Leu Val
115 120 125
Thr Val Cys Pro Val Val Val Val Gly Lys Ala Pro Ala Val Gln Val
130 135 140
His Thr Ser Val Pro Asp Val Leu Ser Pro Leu Ser Gly Asp Glu Ala
145 150 155 160
Lys Ile Gln Ile Leu Gln His Ile Glu Arg Ala Ser Gly Ser Ile Ser
165 170 175
Leu Val His Val Asp Asp Leu Cys Arg Ala Glu Val Phe Leu Ala Glu
180 185 190
Glu Glu Ala Val Ala Ser Gly Arg Tyr Ile Cys Cys Ser Leu Ser Thr
195 200 205
Thr Ala Gly Val Leu Ala Arg Phe Leu Ser Val Lys Tyr Pro Gln Tyr
210 215 220
Lys Val Arg Thr Asp Arg Phe Ser Gly Ser Pro Glu Lys Pro Arg Val
225 230 235 240
Cys Met Ser Ser Ala Lys Leu Val Ala Glu Gly Phe Gln Tyr Lys Tyr
245 250 255
Lys Thr Leu Asp Glu Ile Tyr Asp Asp Val Val Glu Tyr Gly Arg Ala

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            260                      265                      270
Leu Gly Ile Leu Pro
        275

&lt;210&gt; 79
&lt;211&gt; 342
&lt;212&gt; PRT
&lt;213&gt; Festuca arundinacea

&lt;400&gt; 79
Met Ala Ala Ala Gly Asp Gly Ser Arg Arg Lys Thr Ala Cys Val Thr
 1               5                  10                  15
Gly Gly Asn Gly Tyr Ile Ala Ser Ala Leu Val Lys Met Leu Leu Glu
            20                  25                  30
Lys Gly Tyr Ala Val Lys Thr Thr Val Arg Asn Pro Asp Asp Met Glu
        35                  40                  45
Lys Asn Ser His Leu Lys Asp Leu Gln Ala Leu Gly Pro Leu Glu Val
    50                  55                  60
Phe Arg Ala Asp Leu Gln Glu Glu Gly Ser Phe Asp Asp Ala Val Ala
65                  70                  75                  80
Gly Cys Asp Tyr Ala Phe Leu Val Ala Ala Pro Val Asn Leu Lys Ala
                85                  90                  95
Glu Asn Pro Glu Lys Asp Met Val Glu Pro Ala Val Gly Gly Thr Leu
            100                 105                 110
Asn Ala Met Arg Ser Cys Val Arg Ala Gly Thr Val Lys Arg Val Val
        115                 120                 125
Leu Thr Ser Ser Val Ala Ser Val Ser Ala Arg Pro Leu Leu Gln Gly
    130                 135                 140
Asp Gly His Val Leu Asp Glu Glu Ser Trp Ser Asp Val Asp Phe Leu
145                 150                 155                 160
Arg Ala Lys Ala Thr Gly His Trp Gly Tyr Pro Val Ser Lys Val Leu
                165                 170                 175
Leu Glu Lys Ala Ala Cys Ala Phe Ala Gln Ala Ser Gly Ile Ser Leu
            180                 185                 190
Val Thr Val Cys Pro Val Val Val Val Gly Lys Ala Pro Ala Val Gln
        195                 200                 205
Val His Thr Ser Val Pro Asp Val Leu Ser Pro Leu Ser Gly Asp Glu
    210                 215                 220
Ala Lys Ile Gln Ile Leu Gln His Ile Glu Arg Ala Ser Gly Ser Ile
225                 230                 235                 240
Ser Leu Val His Val Asp Asp Leu Cys Arg Ala Glu Val Phe Leu Ala
                245                 250                 255
Glu Glu Glu Ala Val Ala Ser Gly Arg Tyr Ile Cys Cys Ser Leu Ser
            260                 265                 270
Thr Thr Ala Gly Val Leu Ala Arg Phe Leu Ser Val Lys Tyr Pro Gln
        275                 280                 285
Tyr Lys Val Arg Thr Asp Arg Phe Ser Gly Ser Pro Glu Lys Pro Arg
    290                 295                 300
Val Cys Met Ser Ser Ala Lys Leu Val Ala Glu Gly Phe Gln Tyr Lys
305                 310                 315                 320
Tyr Lys Thr Leu Asp Glu Ile Tyr Asp Asp Val Val Glu Tyr Gly Arg
                325                 330                 335
Ala Leu Gly Ile Leu Pro
            340

&lt;210&gt; 80
&lt;211&gt; 255
&lt;212&gt; PRT
&lt;213&gt; Lolium perenne

&lt;400&gt; 80
Phe Ile Ser Val Thr Val Phe Tyr Val Val Gly Leu Arg Gln Arg Asp
 1               5                  10                  15
Leu Val Gln Ala Gly Val Gln Gly Thr Leu Asn Val Met Arg Ser Cys
            20                  25                  30
Val Lys Ala Gly Thr Val Lys Arg Val Ile Leu Thr Ser Ser Asp Ser
        35                  40                  45
Ala Val Cys Gln Arg Pro Leu Glu Gly Asp Gly His Val Leu Asp Glu
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    50                  55                  60
Gly Ser Trp Ser Asp Val Pro Tyr Leu Arg Ala Glu Gln Pro Glu Ala
65                  70                  75                  80
Trp Gly Tyr Ala Val Ser Lys Val Leu Met Glu Glu Ala Ala Gly Lys
                85                  90                  95
Phe Ala Asp Glu Asn Gly Leu Gly Leu Val Ser Val Leu Pro Thr Phe
            100                 105                 110
Thr Leu Gly Ala Ala Pro Val Ser Gln Ala Arg Thr Ser Val Pro Val
        115                 120                 125
Val Leu Ser Leu Leu Ser Gly Asp Glu Glu Gln Leu Asn Leu Leu Glu
    130                 135                 140
Ala Met His Leu Ile Thr Glu Ser Val Ser Ile Asn His Ile Asp Asp
145                 150                 155                 160
Leu Cys Arg Ala Gln Val Phe Leu Ala Glu Asn Glu Ala Ser Ser Gly
                165                 170                 175
Arg Tyr Ile Cys Ser Ser His Asp Thr Thr Val Val Gln Leu Ala Arg
            180                 185                 190
Leu Leu Ala Asp Lys Tyr Pro Gln Tyr Asn Val Lys Ser Gln Arg Phe
        195                 200                 205
Asp Gly Ser Pro Glu Lys Pro Arg Val Cys Leu Ser Ser Gln Lys Leu
    210                 215                 220
Ile Gly Glu Gly Phe Val Tyr Lys Tyr Asp Asp Leu Gly Ala Ile Leu
225                 230                 235                 240
Asp Asp Leu Val Glu Tyr Gly Arg Thr Thr Gly Ile Leu Pro Phe
                245                 250                 255

<210> 81
<211> 340
<212> PRT
<213> Lolium perenne

<400> 81
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 1               5                  10                  15
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            20                  25                  30
Gly Tyr Ala Val Lys Thr Thr Val Arg Asn Pro Asp Asp Leu Glu Lys
        35                  40                  45
Thr Ser His Leu Lys Asp Leu Gln Ala Phe Gly Pro Leu Glu Ile Phe
    50                  55                  60
Arg Gly Glu Leu Asp Val Glu Gly Ser Phe Asp Asp Ser Val Ser Gly
65                  70                  75                  80
Cys Asp Tyr Val Phe Leu Val Ala Ala Pro Met Asp Met Gly Ser Leu
                85                  90                  95
Asn Pro Glu Arg Asp Leu Val Gln Ala Gly Val Gln Gly Thr Leu Asn
            100                 105                 110
Val Met Arg Ser Cys Val Lys Ala Gly Thr Val Lys Arg Val Ile Leu
        115                 120                 125
Thr Ser Ser Asp Ser Ala Val Cys Gln Arg Pro Leu Glu Gly Asp Gly
    130                 135                 140
His Val Leu Asp Glu Gly Ser Trp Ser Asp Val Pro Tyr Leu Arg Ala
145                 150                 155                 160
Glu Gln Pro Glu Ala Trp Gly Tyr Ala Val Ser Lys Val Leu Met Glu
                165                 170                 175
Glu Ala Ala Gly Lys Phe Ala Asp Glu Asn Gly Leu Gly Leu Val Ser
            180                 185                 190
Val Leu Pro Thr Phe Thr Leu Gly Ala Ala Pro Val Ser Gln Ala Arg
        195                 200                 205
Thr Ser Val Pro Val Val Leu Ser Leu Leu Ser Gly Asp Glu Glu Gln
    210                 215                 220
Leu Asn Leu Leu Glu Ala Met His Leu Ile Thr Glu Ser Val Ser Ile
225                 230                 235                 240
Asn His Ile Asp Asp Leu Cys Arg Ala Gln Val Phe Leu Ala Glu Asn
                245                 250                 255
Glu Ala Ser Ser Gly Arg Tyr Ile Cys Ser Ser His Asp Thr Thr Val
            260                 265                 270
Val Gln Leu Ala Arg Leu Leu Ala Asp Lys Tyr Pro Gln Tyr Asn Val
        275                 280                 285
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Lys Ser Gln Arg Phe Asp Gly Ser Pro Glu Lys Pro Arg Val Cys Leu
290 295 300
Ser Ser Gln Lys Leu Ile Gly Glu Gly Phe Val Tyr Lys Tyr Asp Asp
305 310 315 320
Leu Gly Ala Ile Leu Asp Asp Leu Val Glu Tyr Gly Arg Thr Thr Gly
325 330 335
Ile Leu Pro Phe
340

<210> 82
<211> 508
<212> PRT
<213> Lolium perenne

<400> 82
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20 25 30
Leu Gly Asn Leu Pro Gln Val Gly Ala Lys Pro His His Thr Met Ala
35 40 45
Ala Leu Ser Gln Gln Phe Gly Pro Leu Phe Arg Leu Arg Phe Gly Val
50 55 60
Ala Glu Val Val Val Ala Ala Ser Ala Lys Val Ala Ser Gln Phe Leu
65 70 75 80
Arg Ala His Asp Ala Asn Phe Ser Asp Arg Pro Pro Asn Ser Gly Ala
85 90 95
Glu His Val Ala Tyr Asn Tyr Gln Asp Leu Val Phe Ala Pro Tyr Gly
100 105 110
Ser Arg Trp Arg Ala Leu Arg Lys Leu Cys Ala Leu His Leu Phe Ser
115 120 125
Ala Lys Ala Leu Asp Ala Leu Arg Ala Val Arg Glu Ala Glu Val Ala
130 135 140
Leu Met Val Lys Gln Leu Lys Glu Ser Ala Pro Ala Gly Val Val Val
145 150 155 160
Gly Gln Glu Ala Asn Val Cys Ala Thr Asn Ala Leu Ala Arg Ala Ala
165 170 175
Val Gly Arg Arg Val Phe Gly Gly Ser Ala Gly Glu Gly Ala Arg Glu
180 185 190
Phe Lys Asp Met Val Val Glu Leu Met Gln Leu Ala Gly Val Phe Asn
195 200 205
Ile Gly Asp Phe Val Pro Ala Leu Arg Trp Leu Asp Pro Gln Gly Val
210 215 220
Val Ala Arg Met Lys Arg Leu His Arg Arg Tyr Asp Ala Met Met Asp
225 230 235 240
Gly Phe Ile Ser Glu Arg Asp Gln Arg His Asn Gln Ala Ala Ala Asp
245 250 255
Gly Glu Arg Lys Asp Leu Leu Ser Val Met Leu Gly Tyr Met Arg Pro
260 265 270
Asp Gly Gly Gly Gly Glu Glu Glu Gly Ile Ser Phe Asn His Thr Asp
275 280 285
Ile Lys Ala Leu Leu Leu Asn Leu Phe Thr Ala Gly Thr Asp Thr Thr
290 295 300
Ser Ser Thr Val Glu Trp Ala Leu Ala Glu Leu Ile Arg His Lys Asp
305 310 315 320
Val Leu Thr Gln Ala Gln Arg Glu Leu Asp Asp Ile Val Gly Gln Asp
325 330 335
Arg Leu Val Thr Glu Ser Asp Leu Pro His Leu Thr Phe Leu Thr Ala
340 345 350
Val Ile Lys Glu Thr Phe Arg Leu His Pro Ser Thr Pro Leu Ser Leu
355 360 365
Pro Arg Val Ala Thr Glu Asp Cys Glu Val Glu Gly Tyr Arg Ile Pro
370 375 380
Lys Gly Thr Thr Leu Leu Val Asn Val Trp Ala Ile Ala Arg Asp Pro
385 390 395 400
Ala Ser Trp Gly Pro Asp Ala Leu Glu Phe Arg Pro Ala Arg Phe Leu
405 410 415
Ala Gly Gly Leu His Glu Ser Val Asp Val Lys Gly Ser Asp Tyr Glu

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            420                     425                     430
Leu Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala Gly Leu Ser Trp
        435                     440                     445
Gly Leu Arg Met Val Thr Leu Met Thr Ala Thr Leu Val His Ala Phe
    450                     455                     460
Asp Trp Ser Leu Val Asp Gly Leu Thr Pro Glu Lys Leu Asp Met Glu
465                     470                     475                     480
Glu Ala Tyr Gly Leu Thr Leu Gln Arg Ala Ala Pro Leu Met Val Arg
                485                     490                     495
Pro Ile Pro Arg Leu Leu Ser Ser Ala Tyr Thr Val
            500                     505

<210> 83
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<212> PRT
<213> Lolium perenne

<400> 83
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Lys Leu Ser Lys Leu Pro Leu Pro Pro Gly Pro Arg Gly Trp Pro Val
        35                  40                  45
Leu Gly Asn Leu Pro Gln Val Gly Ala Lys Pro His His Thr Met Ala
    50                  55                  60
Ala Leu Ser Gln Gln Phe Gly Pro Leu Phe Arg Leu Arg Phe Gly Val
65                  70                  75                  80
Ala Glu Val Val Val Ala Ala Ser Ala Lys Val Ala Ser Gln Phe Leu
                85                  90                  95
Arg Ala His Asp Ala Asn Phe Ser Asp Arg Pro Pro Asn Ser Gly Ala
            100                 105                 110
Glu His Val Ala Tyr Asn Tyr Gln Asp Leu Val Phe Ala Pro Tyr Gly
        115                 120                 125
Ser Arg Trp Arg Ala Leu Arg Lys Leu Cys Ala Leu His Leu Phe Ser
    130                 135                 140
Ala Lys Ala Leu Asp Ala Leu Arg Ala Val Arg Glu Ala Glu Val Ala
145                 150                 155                 160
Leu Met Val Lys Gln Leu Lys Glu Ser Ala Pro Ala Gly Val Val Val
                165                 170                 175
Gly Gln Glu Ala Asn Val Cys Ala Thr Asn Ala Leu Ala Arg Ala Ala
            180                 185                 190
Val Gly Arg Arg Val Phe Gly Gly Ser Ala Gly Glu Gly Ala Arg Glu
        195                 200                 205
Phe Lys Asp Met Val Val Glu Leu Met Gln Leu Ala Gly Val Phe Asn
    210                 215                 220
Ile Gly Asp Phe Val Pro Ala Leu Arg Trp Leu Asp Pro Gln Gly Val
225                 230                 235                 240
Val Ala Arg Met Lys Arg Leu His Arg Arg Tyr Asp Ala Met Met Asp
                245                 250                 255
Gly Phe Ile Ser Glu Arg Asp Gln Arg His Asn Gln Ala Ala Ala Asp
            260                 265                 270
Gly Glu Arg Lys Asp Leu Leu Ser Val Met Leu Gly Tyr Met Arg Pro
        275                 280                 285
Asp Gly Gly Gly Gly Glu Glu Glu Gly Ile Ser Phe Asn His Thr Asp
    290                 295                 300
Ile Lys Ala Leu Leu Leu Asn Leu Phe Thr Ala Gly Thr Asp Thr Thr
305                 310                 315                 320
Ser Ser Thr Val Glu Trp Ala Leu Ala Glu Leu Ile Arg His Lys Asp
                325                 330                 335
Val Leu Thr Gln Ala Gln Arg Glu Leu Asp Asp Ile Val Gly Gln Asp
            340                 345                 350
Arg Leu Val Thr Glu Ser Asp Leu Pro His Leu Thr Phe Leu Thr Ala
        355                 360                 365
Val Ile Lys Glu Thr Phe Arg Leu His Pro Ser Thr Pro Leu Ser Leu
    370                 375                 380
Pro Arg Val Ala Thr Glu Asp Cys Glu Val Glu Gly Tyr Arg Ile Pro
385                 390                 395                 400
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Lys Gly Thr Thr Leu Leu Val Asn Val Trp Ala Ile Ala Arg Asp Pro
405 410 415
Ala Ser Trp Gly Pro Asp Ala Leu Glu Phe Arg Pro Ala Arg Phe Leu
420 425 430
Ala Gly Gly Leu His Glu Ser Val Asp Val Lys Gly Ser Asp Tyr Glu
435 440 445
Leu Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala Gly Leu Ser Trp
450 455 460
Gly Leu Arg Met Val Thr Leu Met Thr Ala Thr Leu Val His Ala Phe
465 470 475 480
Asp Trp Ser Leu Val Asp Gly Leu Thr Pro Glu Lys Leu Asp Met Glu
485 490 495
Glu Ala Tyr Gly Leu Thr Leu Gln Arg Ala Ala Pro Leu Met Val Arg
500 505 510
Pro Ile Pro Arg Leu Leu Ser Ser Ala Tyr Thr Val
515 520

<210> 84
<211> 525
<212> PRT
<213> Festuca arundinacea

<400> 84
Arg Ser Glu Leu Ala Gly Met Asp Ile Pro Leu Ser Leu Leu Leu Ser
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Thr Leu Ala Ile Ser Ala Thr Ile Cys Tyr Val Phe Phe Arg Ala Gly
20 25 30
Lys Gly His Arg Ala Pro Leu Pro Leu Pro Pro Gly Pro Arg Gly Trp
35 40 45
Pro Val Leu Gly Asn Leu Pro Gln Leu Gly Gly Lys Thr His Gln Thr
50 55 60
Leu His Glu Met Thr Lys Val Tyr Gly Pro Val Leu Arg Leu Arg Phe
65 70 75 80
Gly Ser Ser Val Val Val Val Ala Gly Ser Ala Ala Val Ala Glu Gln
85 90 95
Phe Leu Arg Thr His Asp Ala Lys Phe Ser Ser Arg Pro Pro Asn Ser
100 105 110
Gly Gly Glu His Met Ala Tyr Asn Tyr Arg Asp Val Val Phe Ala Pro
115 120 125
Tyr Gly Pro Arg Trp Arg Ala Met Arg Lys Val Cys Ala Val Asn Ile
130 135 140
Phe Ser Ala Arg Ala Leu Asp Asp Leu Arg Gly Phe Arg Glu Arg Glu
145 150 155 160
Ala Ala Leu Met Val Arg Ser Leu Ala Asp Ala Ala Lys Ala Gly Val
165 170 175
Ala Val Ala Val Gly Lys Ala Ala Asn Val Cys Thr Thr Asn Gly Leu
180 185 190
Ser Arg Ala Ala Val Gly Leu Arg Val Phe Gly Ser Asp Gly Ala Arg
195 200 205
Asp Phe Lys Glu Ile Val Leu Glu Val Met Glu Val Gly Gly Val Leu
210 215 220
Asn Val Gly Asp Phe Val Pro Ala Leu Arg Trp Leu Asp Pro Gln Gly
225 230 235 240
Val Val Ala Arg Leu Lys Lys Leu His Arg Arg Phe Asp Asp Met Met
245 250 255
Asn Gly Ile Ile Ala Glu Arg Arg Thr Gly Thr Lys Thr Ala Val Val
260 265 270
Glu Glu Gly Lys Gly Asp Leu Leu Gly Leu Leu Leu Ala Met Val Gln
275 280 285
Glu Asp Lys Ser Leu Thr Gly Ser Glu Glu Asp Lys Ile Thr Asp Thr
290 295 300
Asp Val Lys Ala Leu Ile Leu Asn Leu Phe Val Ala Gly Thr Glu Thr
305 310 315 320
Thr Ser Ser Ile Val Glu Trp Ala Val Ala Glu Leu Ile Arg His Pro
325 330 335
Asp Ile Leu Lys Gln Ala Gln Glu Glu Leu Asp Ala Val Val Gly Arg
340 345 350
Asp Arg Leu Val Ser Glu Ser Asp Leu Pro Arg Leu Thr Phe Phe Asn

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                355                     360                     365
Ala Ile Ile Lys Glu Thr Phe Arg Leu His Pro Ser Thr Pro Leu Ser
    370                     375                     380
Leu Pro Arg Met Ala Ser Glu Glu Cys Glu Val Ala Gly Tyr His Ile
385                     390                     395                     400
Pro Arg Gly Thr Glu Leu Leu Val Asn Val Trp Gly Ile Ala Arg Asp
                405                     410                     415
Pro Ala Leu Trp Pro Asp Pro Leu Glu Tyr Gln Pro Ala Arg Phe Leu
            420                     425                     430
Pro Gly Gly Ser His Glu Asn Val Asp Leu Lys Gly Gly Asp Phe Gly
        435                     440                     445
Leu Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala Gly Leu Ser Trp
    450                     455                     460
Gly Leu Arg Met Val Thr Ile Thr Thr Ala Thr Leu Val His Ser Phe
465                     470                     475                     480
Asp Trp Glu Leu Pro Ala Gly Gln Thr Pro Asp Lys Leu Asn Met Glu
                485                     490                     495
Glu Ala Phe Ser Leu Leu Leu Gln Arg Ala Val Pro Leu Met Val His
            500                     505                     510
Pro Val Pro Arg Leu Leu Pro Ser Ala Tyr Glu Ile Ser
        515                     520                     525

&lt;210&gt; 85
&lt;211&gt; 526
&lt;212&gt; PRT
&lt;213&gt; Festuca arundinacea

&lt;400&gt; 85
Met Arg Ser Glu Leu Ala Gly Met Asp Ile Pro Leu Pro Leu Leu Leu
1               5                   10                  15
Ser Thr Leu Ala Ile Ser Ala Thr Ile Cys Tyr Val Phe Phe Arg Ala
            20                  25                  30
Gly Lys Gly His Arg Ala Pro Leu Pro Leu Pro Pro Gly Pro Arg Gly
        35                  40                  45
Trp Pro Val Leu Gly Asn Leu Pro Gln Leu Gly Gly Lys Thr His Gln
    50                  55                  60
Thr Leu His Glu Met Thr Lys Val Tyr Gly Pro Val Leu Arg Leu Arg
65                  70                  75                  80
Phe Gly Ser Ser Val Val Val Val Ala Gly Ser Ala Ala Val Ala Glu
                85                  90                  95
Gln Phe Leu Arg Thr His Asp Ala Lys Phe Ser Ser Arg Pro Pro Asn
            100                 105                 110
Ser Gly Gly Glu His Met Ala Tyr Asn Tyr Arg Asp Val Val Phe Ala
        115                 120                 125
Pro Tyr Gly Pro Arg Trp Arg Ala Met Arg Lys Val Cys Ala Val Asn
    130                 135                 140
Ile Phe Ser Ala Arg Ala Leu Asp Asp Leu Arg Gly Phe Arg Glu Arg
145                 150                 155                 160
Glu Ala Ala Leu Met Val Arg Ser Leu Ala Asp Ala Ala Lys Ala Gly
                165                 170                 175
Val Ala Val Ala Val Gly Lys Ala Ala Asn Val Cys Thr Thr Asn Gly
            180                 185                 190
Leu Ser Arg Ala Ala Val Gly Leu Arg Val Phe Gly Ser Asp Gly Ala
        195                 200                 205
Arg Asp Phe Lys Glu Ile Val Leu Glu Val Met Glu Val Gly Gly Val
    210                 215                 220
Leu Asn Val Gly Asp Phe Val Pro Ala Leu Arg Trp Leu Asp Pro Gln
225                 230                 235                 240
Gly Val Val Ala Arg Leu Lys Lys Leu His Arg Arg Phe Asp Asp Met
                245                 250                 255
Met Asn Gly Ile Ile Ala Glu Arg Arg Thr Gly Thr Lys Thr Ala Val
            260                 265                 270
Val Glu Glu Gly Lys Gly Asp Leu Leu Gly Leu Leu Leu Ala Met Val
        275                 280                 285
Gln Glu Asp Lys Ser Leu Thr Gly Ser Glu Glu Asp Lys Ile Thr Asp
    290                 295                 300
Thr Asp Val Lys Ala Leu Ile Leu Asn Leu Phe Val Ala Gly Thr Glu
305                 310                 315                 320
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Thr Thr Ser Ser Ile Val Glu Trp Ala Val Ala Glu Leu Ile Arg His
325 330 335
Pro Asp Ile Leu Lys Gln Ala Gln Glu Glu Leu Asp Ala Val Val Gly
340 345 350
Arg Asp Arg Leu Val Ser Glu Ser Asp Leu Pro Arg Leu Thr Phe Phe
355 360 365
Asn Ala Ile Ile Lys Glu Thr Phe Arg Leu His Pro Ser Thr Pro Leu
370 375 380
Ser Leu Pro Arg Met Ala Ser Glu Glu Cys Glu Val Ala Gly Tyr His
385 390 395 400
Ile Pro Arg Gly Thr Glu Leu Leu Val Asn Val Trp Gly Ile Ala Arg
405 410 415
Asp Pro Ala Leu Trp Pro Asp Pro Leu Glu Tyr Gln Pro Ala Arg Phe
420 425 430
Leu Pro Gly Gly Ser His Glu Asn Val Asp Leu Lys Gly Gly Asp Phe
435 440 445
Gly Leu Ile Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala Gly Leu Ser
450 455 460
Trp Gly Leu Arg Met Val Thr Ile Thr Thr Ala Thr Leu Val His Ser
465 470 475 480
Phe Asp Trp Glu Leu Pro Ala Gly Gln Thr Pro Asp Lys Leu Asn Met
485 490 495
Glu Glu Ala Phe Ser Leu Leu Leu Gln Arg Ala Val Pro Leu Met Val
500 505 510
His Pro Val Pro Arg Leu Leu Pro Ser Ala Tyr Glu Ile Ser
515 520 525

<210> 86
<211> 491
<212> PRT
<213> Festuca arundinacea

<400> 86
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Ile Cys Tyr Val Phe Phe Arg Ala Gly Lys Thr His Gln Thr Leu His
20 25 30
Glu Met Thr Lys Val Tyr Gly Pro Val Leu Arg Leu Arg Phe Gly Ser
35 40 45
Ser Val Val Val Val Ala Gly Ser Ala Ala Val Ala Glu Gln Phe Leu
50 55 60
Arg Thr His Asp Ala Lys Phe Ser Ser Arg Pro Pro Asn Ser Gly Gly
65 70 75 80
Glu His Met Ala Tyr Asn Tyr Gln Asp Ile Val Phe Ala Pro Tyr Gly
85 90 95
Pro Arg Trp Arg Ala Met Arg Lys Val Cys Ala Val Asn Ile Phe Ser
100 105 110
Ala Arg Ala Leu Asp Asp Leu Arg Gly Phe Arg Glu Arg Glu Ala Ala
115 120 125
Leu Met Val Arg Ser Leu Ala Asp Ala Ala Lys Ala Gly Ala Ala Val
130 135 140
Ala Val Gly Lys Ala Ala Asn Val Cys Thr Thr Asn Gly Leu Ser Arg
145 150 155 160
Ala Ala Val Gly Leu Arg Val Phe Gly Ser Asp Gly Thr Arg Asp Phe
165 170 175
Lys Glu Ile Val Leu Glu Val Met Glu Val Gly Gly Val Leu Asn Val
180 185 190
Gly Asp Phe Val Pro Ala Leu Arg Trp Leu Asp Pro Gln Gly Val Val
195 200 205
Ala Arg Met Lys Lys Leu His Arg Arg Phe Asp Asp Ile Met Asn Gly
210 215 220
Ile Ile Ala Glu Arg Arg Thr Gly Ala Lys Thr Ala Val Val Glu Glu
225 230 235 240
Gly Lys Gly Asp Leu Leu Gly Leu Leu Leu Ala Met Val Gln Glu Asp
245 250 255
Lys Ser Leu Thr Gly Ser Glu Glu Asp Lys Ile Thr Asp Thr Asp Val
260 265 270
Lys Ala Leu Ile Leu Asn Leu Phe Val Ala Gly Thr Glu Thr Thr Ser

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            275                     280                     285
Ser Ile Val Glu Trp Ala Val Ala Glu Leu Ile Arg His Pro Asp Ile
        290                     295                     300
Leu Lys Gln Ala Gln Glu Glu Leu Asp Thr Val Val Gly Arg Asp Arg
305                     310                     315                     320
Ile Val Ser Glu Ser Asp Leu Pro Arg Leu Thr Phe Phe Asn Ala Ile
                325                     330                     335
Ile Lys Glu Thr Phe Arg Leu His Pro Ser Thr Pro Leu Ser Leu Pro
            340                     345                     350
Arg Met Ala Ser Glu Asp Cys Glu Val Ala Gly Tyr His Ile Pro Arg
        355                     360                     365
Gly Thr Glu Leu Leu Val Asn Val Trp Gly Ile Ala Arg Asp Pro Ser
    370                     375                     380
Leu Trp Pro Asp Pro Leu Glu Tyr Arg Pro Ala Arg Phe Leu Pro Gly
385                     390                     395                     400
Gly Ser His Glu Asn Val Asp Leu Lys Gly Gly Asp Phe Gly Leu Ile
                405                     410                     415
Pro Phe Gly Ala Gly Arg Arg Ile Cys Ala Gly Leu Ser Trp Gly Leu
            420                     425                     430
Arg Met Val Thr Val Thr Thr Ala Thr Leu Val His Ser Phe Asp Trp
        435                     440                     445
Glu Leu Pro Ala Gly Gln Thr Leu Asp Lys Leu Asn Met Glu Glu Ala
    450                     455                     460
Phe Ser Leu Leu Leu Gln Arg Ala Met Pro Leu Met Val His Pro Val
465                     470                     475                     480
Pro Arg Leu Leu Pro Ser Ala Tyr Glu Ile Ser
                485                     490
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<210> 87
<211> 499
<212> PRT
<213> Festuca arundinacea

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<400> 87
Met Arg Asn Glu Leu Ala Gly Met Asp Ile Pro Leu Pro Leu Leu Leu
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Ser Thr Leu Ala Ile Ser Ala Thr Ile Cys Tyr Val Phe Phe Arg Ala
            20                  25                  30
Gly Lys Thr His Gln Thr Leu His Glu Met Thr Lys Val Tyr Gly Pro
        35                  40                  45
Val Leu Arg Leu Arg Phe Gly Ser Ser Val Val Val Val Ala Gly Ser
    50                  55                  60
Ala Ala Val Ala Glu Gln Phe Leu Arg Thr His Asp Ala Lys Phe Ser
65                  70                  75                  80
Ser Arg Pro Pro Asn Ser Gly Gly Glu His Met Ala Tyr Asn Tyr Gln
                85                  90                  95
Asp Ile Val Phe Ala Pro Tyr Gly Pro Arg Trp Arg Ala Met Arg Lys
            100                 105                 110
Val Cys Ala Val Asn Ile Phe Ser Ala Arg Ala Leu Asp Asp Leu Arg
        115                 120                 125
Gly Phe Arg Glu Arg Glu Ala Ala Leu Met Val Arg Ser Leu Ala Asp
    130                 135                 140
Ala Ala Lys Ala Gly Ala Ala Val Ala Val Gly Lys Ala Ala Asn Val
145                 150                 155                 160
Cys Thr Thr Asn Gly Leu Ser Arg Ala Ala Val Gly Leu Arg Val Phe
                165                 170                 175
Gly Ser Asp Gly Thr Arg Asp Phe Lys Glu Ile Val Leu Glu Val Met
            180                 185                 190
Glu Val Gly Gly Val Leu Asn Val Gly Asp Phe Val Pro Ala Leu Arg
        195                 200                 205
Trp Leu Asp Pro Gln Gly Val Val Ala Arg Met Lys Lys Leu His Arg
    210                 215                 220
Arg Phe Asp Asp Ile Met Asn Gly Ile Ile Ala Glu Arg Arg Thr Gly
225                 230                 235                 240
Ala Lys Thr Ala Val Val Glu Glu Gly Lys Gly Asp Leu Leu Gly Leu
                245                 250                 255
Leu Leu Ala Met Val Gln Glu Asp Lys Ser Leu Thr Gly Ser Glu Glu
            260                 265                 270
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Asp Lys Ile Thr Asp Thr Asp Val Lys Ala Leu Ile Leu Asn Leu Phe
275 280 285
Val Ala Gly Thr Glu Thr Thr Ser Ser Ile Val Glu Trp Ala Val Ala
290 295 300
Glu Leu Ile Arg His Pro Asp Ile Leu Lys Gln Ala Gln Glu Glu Leu
305 310 315 320
Asp Thr Val Val Gly Arg Asp Arg Ile Val Ser Glu Ser Asp Leu Pro
325 330 335
Arg Leu Thr Phe Phe Asn Ala Ile Ile Lys Glu Thr Phe Arg Leu His
340 345 350
Pro Ser Thr Pro Leu Ser Leu Pro Arg Met Ala Ser Glu Asp Cys Glu
355 360 365
Val Ala Gly Tyr His Ile Pro Arg Gly Thr Glu Leu Leu Val Asn Val
370 375 380
Trp Gly Ile Ala Arg Asp Pro Ser Leu Trp Pro Asp Pro Leu Glu Tyr
385 390 395 400
Arg Pro Ala Arg Phe Leu Pro Gly Gly Ser His Glu Asn Val Asp Leu
405 410 415
Lys Gly Gly Asp Phe Gly Leu Ile Pro Phe Gly Ala Gly Arg Arg Ile
420 425 430
Cys Ala Gly Leu Ser Trp Gly Leu Arg Met Val Thr Val Thr Thr Ala
435 440 445
Thr Leu Val His Ser Phe Asp Trp Glu Leu Pro Ala Gly Gln Thr Leu
450 455 460
Asp Lys Leu Asn Met Glu Glu Ala Phe Ser Leu Leu Leu Gln Arg Ala
465 470 475 480
Met Pro Leu Met Val His Pro Val Pro Arg Leu Leu Pro Ser Ala Tyr
485 490 495
Glu Ile Ser

<210> 88
<211> 380
<212> PRT
<213> Lolium perenne

<400> 88
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20 25 30
Val Lys Pro Pro Arg Asp Arg Pro Ala Ala Gln His Leu Ala Thr Ala
35 40 45
Ala Ser Ala Asp Gly Asp Val Leu His Glu Pro Leu Asp Thr Ser Ile
50 55 60
Pro Val Ile Asp Leu Gly Glu Leu Val Ala Ala Thr Ala Asp Glu Gly
65 70 75 80
Arg Met Arg Gln Ile Met Glu Ala Val Ala Ala Ala Cys Arg Glu Trp
85 90 95
Gly Phe Phe Gln Val Val Asn His Gly Val Ala Pro Glu Leu Met His
100 105 110
Ala Ala Arg Glu Ala Trp Arg Gly Phe Phe Arg Leu Pro Ile Thr Ala
115 120 125
Lys Gln Gln Tyr Ala Asn Leu Pro Arg Thr Tyr Glu Gly Tyr Gly Ser
130 135 140
Arg Val Gly Val Gln Lys Gly Gly Pro Leu Asp Trp Gly Asp Tyr Tyr
145 150 155 160
Phe Leu His Leu Ala Pro Asp Ala Gly Lys Ser Pro Asp Lys Tyr Trp
165 170 175
Pro Thr Asn Pro Ala Ile Cys Lys Asp Val Ser Glu Glu Tyr Gly Arg
180 185 190
Glu Val Ile Arg Leu Cys Glu Leu Leu Met Lys Val Met Ser Ala Ser
195 200 205
Leu Gly Leu Glu Ala Thr Arg Phe Gln Glu Ala Phe Gly Gly Ser Glu
210 215 220
Cys Gly Val Cys Leu Arg Ala Asn Tyr Tyr Pro Arg Cys Pro Gln Pro
225 230 235 240
Asp Leu Thr Leu Gly Leu Ser Ala His Ser Asp Pro Gly Val Leu Thr

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                    245                     250                     255
Val Leu Leu Ala Asp Glu His Val Arg Gly Leu Gln Val Arg Arg Ala
                260                 265                 270
Asp Gly Glu Trp Val Thr Val Gln Pro Ala Arg His Asp Ala Phe Ile
            275                 280                 285
Val Asn Val Gly Asp Gln Ile Gln Ile Leu Ser Asn Ser Met Tyr Lys
    290                 295                 300
Ser Val Glu His Arg Val Met Val Asn Ala Lys Glu Glu Arg Ile Ser
305                 310                 315                     320
Leu Ala Leu Phe Tyr Asn Pro Arg Gly Asp Val Pro Ile Ala Pro Ala
                325                 330                     335
Pro Glu Thr Val Thr Pro Glu Arg Pro Ala Leu Tyr Pro Ser Met Thr
            340                 345                 350
Phe Asp Glu Tyr Arg Ala Tyr Ile Arg Lys Tyr Gly Pro Arg Gly Lys
        355                 360                 365
Ala Gln Val Glu Gly Ala Lys Gln Gly Gln Gly Ser
    370                 375                 380
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<210> 89
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in the lab

<400> 89
gacgcaagga gagatccaga 20

<210> 90
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in the lab

<400> 90
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<210> 91
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in the lab

<400> 91
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<210> 92
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Made in the lab

<400> 92
gccgaacaga ccattgaagt a 21

INTERNATIONAL SEARCH REPORT

International application No.
PCT/NZ03/00081

A. CLASSIFICATION OF SUBJECT MATTER

Int. Cl. 7: C12N 9/10, 9/02, 5/14, 15/82, C07K 14/415, A01H 5/00

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
See electronic database box below.

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched
See electronic database box below.

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
DGENE, EMBL, GenBank, PDB, DDBJ, USPTO sequences: SEQ ID NO: 4, 12, 15, 15, 17, 20, 22, 27, 33, 35, 37.

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	EMBL database Accession Number AF492836 & AAM13671. Lasseur B *et al.* 16 April 2002. "Lolium perenne putative sucrose:sucrose 1-fructosyltransferase mRNA, complete cds". See whole document. 97.8% identical to SEQ ID NOs: 4 and 48.	1-25 (SEQ ID NO: 4 & 48)
X	Luscher M *et al.* (2000) Plant Physiol. 124(3):1217-28. "Cloning and functional analysis of sucrose:sucrose 1-fructosyltransferase from tall fescue". & EMBL database Accession Number AJ297369 & CAC05261. See whole document. 83% identical to SEQ ID NO: 4 and 48.	1-25 (SEQ ID NO: 4 & 48)

[X] Further documents are listed in the continuation of Box C [X] See patent family annex

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance
"E" earlier application or patent but published on or after the international filing date
"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
"O" document referring to an oral disclosure, use, exhibition or other means
"P" document published prior to the international filing date but later than the priority date claimed
"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
22 August 2003	27 AUG 2003

Name and mailing address of the ISA/AU	Authorized officer
AUSTRALIAN PATENT OFFICE PO BOX 200, WODEN ACT 2606, AUSTRALIA E-mail address: pct@ipaustralia.gov.au Facsimile No. (02) 6285 3929	**JANE MCHENRY** Telephone No : (02) 6283 2091

INTERNATIONAL SEARCH REPORT

International application No.
PCT/NZ03/00081

Box I **Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)**

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos :

   because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos :

   because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claims Nos :

   because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a)

Box II **Observations where unity of invention is lacking (Continuation of item 3 of first sheet)**

This International Searching Authority found multiple inventions in this international application, as follows:

See extra sheet below.

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims

☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:1-25 (in part).

Remark on Protest ☐ The additional search fees were accompanied by the applicant's protest.

☐ No protest accompanied the payment of additional search fees.

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages *(Remove spaces when completed if the page is too long)*	Relevant to claim No.
X	WO 01/95691, A (State of Victoria, Department of Natural Resources and Environment *et al.*) 20 December 2001. See whole document. SST (Figure 11 & SEQ ID NO: 11) is 95% identical to SEQ ID NO: 4.	1-25 (SEQ ID NOs: 4 & 48)
X	WO 02/31130, A (Agriculture Victoria Services Pty Ltd & AGRESEARCH Ltd) 18 April 2002. See whole document. SST (figure 56) is 95% identical to SEQ ID NO: 4. SFT (figure 61) is 98% identical to SEQ ID NO: 4. INV (figure 20) is 64.4% identical to SEQ ID NO: 12. SPS (figures 5, 15 and 17) are 96-99% identical to SEQ ID NO: 20. ST (figures 47 and 49) are 94-96.5% identical to SEQ ID NO: 22.	1-25 (SEQ ID NOs: 4 & 48, 12 & 56, 20 & 64, 22 & 66)
X	US 2001/0051335, A (Lalgudi R V *et al.*) 13 December 2001. See whole document. SEQ ID NO: 5640 is 86.4% identical to SEQ ID NO: 12. SEQ ID NOs: 745 & 4804 are 85.7% and 87.5% respectively identical to SEQ ID NO: 15. SEQ ID NO: 5903 is 83.5% identical to SEQ ID NO: 27.	2-4, 6-10, 12, 13. (SEQ ID NO: 12 & 56, 15 & 59, 27 & 71)
X	EP 1033405, A (Ceres Incorporated Malibu) 6 September 2000. See whole document. SEQ ID NO: 11557 is 74% identical to SEQ ID NO: 12. SEQ ID NO: 43076 & 48532 are 81.3% and 73.3 % respectively identical to SEQ ID NO: 17. SEQ ID NO: 20393 is 38.8% identical to SEQ ID NO: 37, also 100% match over 21 nucleotides (nt100-120 of SEQ ID NO: 20393 matches nt555-575 of SEQ ID NO: 37).	2-4, 6-16. (SEQ ID NO: 12 & 56, 17 & 61, 37 & 81)
X	EMBL database Accession Number: AF095521 & AAC67587. Kapri R & Sadka A. 26 October 1998. "Citrus X paradisi pyrophosphate-dependent phosphofructokinase alpha subunit (PPi-PFKa) mRNA, complete cds". See whole document. 70.6% identical to SEQ ID NO: 15 over entire length, 83% identical over 407 nucleotides (nt 634-1040).	1-25. (SEQ ID NO: 15 & 59)
X	Carlisle S M *et al.* (1990) J Biol. Chem. 265(30): 18366-18371. "Pyrophosphate-dependent phosphofructokinase. Conservation of protein sequence between the alpha- and beta-subunits and with the ATP-dependent phosphofructokinase" & EMBL database Accession Number: M55190 & AAA63451 and M55191 & AAA63452. See whole document. 70.7% identical to SEQ ID NO: 15. 78% identical to SEQ ID NO: 17.	1-25. (SEQ ID NO: 15 & 59, 17 & 61))

C (Continuation)	DOCUMENTS CONSIDERED TO BE RELEVANT	
Category*	Citation of document, with indication, where appropriate, of the relevant passages *(Remove spaces when completed if the page is too long)*	Relevant to claim No.
X	WO 02/16655, A (The Scripps Research Institute *et al.*) 28 February 2002. See whole document. SEQ ID NO: 2691 is 72.2% identical to SEQ ID NO: 15. SEQ ID NO: 188 is 73.3% identical to SEQ ID NO: 17.	1-25 (SEQ ID NO: 15 & 59, 17& 61)
P, X	US 6476212, B (Lalgudi, R V *et al.*) 5 November 2002. See whole document. SEQ ID NO: 584, 1329, 3963, 7175 are 86%, 93%, 87% and 85% identical to SEQ ID NO: 15 respectively.	2-4, 6-14. (SEQ ID NO: 15 & 59)
X	EMBL database Accession Number: AF095520 & AAC67586. Kapri R & Sadka A. 26 October 1998. "Citrus X paradisi pyrophosphate-dependent phosphofructokinase beta subunit (PPi-PFKb) mRNA, complete cds". See whole document. 37.7% identical to SEQ ID NO: 17 over entire length, 82% identical over 620 nucleotides (nt 513-1132 matches nt 541-1160 of SEQ ID NO: 17)	1-25. (SEQ ID NO: 17 & 61)
X	US 2002/0042930, A (Botha F C & Groenewald J H) 11 April 2002. See whole document. Especially figure 2 And SEQ ID NO: 2 83.2% identical to SEQ ID NO: 17.	1-25 (SEQ ID NO: 17 & 61)
P, X	WO 03/000905, A (SYNGENTA PARTICIPATIONS AG) 3 January 2003. See whole document. SEQ ID NO: 179, 587, 1002 are 92%, 87% & 87% identical to SEQ ID NO: 17 respectively.	1-25 (SEQ ID NO: 17 & 61)
X	EMBL database Accession Number: AF261107 & AAF75266. Lunn J E *et al.* 11 June 2000. "Hordeum vulgare sucrose-phosphate synthase mRNA, partial cds". See whole document. 88.6% identical to SEQ ID NO: 20.	1-25 (SEQ ID NO: 20 & 64)
X	WO 99/57285, A (E.I. DU PONT DE NEMOURS AND COMPANY) 11 November 1999. See whole document. SEQ ID NO: 9 & 19 are 85% & 85.4% identical to SEQ ID NO: 20 respectively.	1-25 (SEQ ID NO: 20 & 64)
X	EMBL database Accession Number: AJ272309 & CAB75882. Weschke W *et al.* 22 February 2000. "Hordeum vulgare mRNA for sucrose transporter 1 (Sut1 gene)" See whole document. 83.6% identical to SEQ ID NO: 22.	1-25 (SEQ ID NO: 22 & 66)

C (Continuation)	DOCUMENTS CONSIDERED TO BE RELEVANT	
Category*	Citation of document, with indication, where appropriate, of the relevant passages *(Remove spaces when completed if the page is too long)*	Relevant to claim No.
X	EMBL database Accession Numbers: AF408842, AF408843 & AF408844 (& AAM13408, AAM13409 & AAM13410). Aoki N *et al.* 16 April 2002. "Triticum aestivum sucrose transporter SUT1A, SUT1B, SUT1D mRNA, complete cds" See whole documents. AF408842 is 82.8% identical to SEQ ID NO: 22. AF408843 is 82.9% identical to SEQ ID NO: 22. AF408844 is 81.8% identical to SEQ ID NO: 22.	1-25 (SEQ ID NO: 22 & 66)
X	WO 99/53068, A ((E.I. DU PONT DE NEMOURS AND COMPANY) 21 October 1999. See whole document, especially SEQ ID NO: 19-22. SEQ ID NO: 19 & 21 are 81.5% & 83% identical to SEQ ID NO: 22.	1-25 (SEQ ID NO: 22 & 66)
X	WO 01/64890, A (Pioneer Hi-Bred International, Inc.) 7 September 2001. See whole document, see SEQ ID NO: 8. SEQ ID NO: 8 is 63.3% identical to SEQ ID NO: 27.	2-4, 6-16 (SEQ ID NO: 27 & 71)
X	EMBL database Accession Number: X92547 & CAA63305. Haussuehl K K *et al.* 12 August 1996. "S. cereale mRNA for chalcone synthase". See whole document. 85.5% identical to SEQ ID NO: 33.	1-25 (SEQ ID NO: 33 & 77)
X	EMBL database Accession Number: X58339 & CAA41250. Rohde W E *et al.* 7 November 1991. "H. vulgare CHS gene for chalcone synthase". See whole document. 74.8% identical to SEQ ID NO: 33.	1-25 (SEQ ID NO: 33 & 77)
X	EMBL database Accession Number: AB000801 & BAA19186. Ichikawa H *et al.* 27 March 2001. "Oryza sativa mRNA for chalcone synthase, complete cds". See whole document. 76.3% identical to SEQ ID NO: 33.	1-25 (SEQ ID NO: 33 & 77)
X	WO 02/20548, A (Washington State University Research Foundation) 14 March 2002. See whole document., especially SEQ ID NO:25 SEQ ID NO: 25 is 79.3% identical to SEQ ID NO: 33.	1-25 (SEQ ID NO: 33 & 77)
P, X	WO 02/086146, A (Cornell Research Foundation Inc.) 31 October 2002. See whole document. SEQ ID NO: 46 is 92.4% identical to SEQ ID NO: 33.	1-25 (SEQ ID NO: 33 & 77)

C (Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages *(Remove spaces when completed if the page is too long)*	Relevant to claim No.
X	GENPEPT & GENBANK database Accession Numbers: AAF23859 & AF092912. Devic M *et al.* 11 January 2000. "DFR-like protein [Arabidopsis thaliana]". See whole document. 45.6% identity & 63.6% similarity with SEQ ID NO: 79 43.2% identity & 67.2% similarity with SEQ ID NO: 81	1-25 (SEQ ID NO: 35 & 79, 37 & 81)
X	GENPEPT & GENBANK database Accession Numbers: CAA75998 & Y16042. Bernhardt J *et al.* 30 June 1998. "Dihydroflavonol4-reductase [zea mays]". See whole document. 39.3% identity & 61.6% similarity with SEQ ID NO: 79 38.3% identity & 64.7% similarity with SEQ ID NO: 81	1-25 (SEQ ID NO: 35 & 79, 37 & 81)
X	GENPEPT & GENBANK database Accession Numbers: BAA12723 & D85102. Tanaka Y *et al.* 6 February 1999. "Dihydroflavonol 4-reductase [Rosa hybrid cultivar]". See whole document. 39% identity & 60.9% similarity with SEQ ID NO: 79 40.2% identity & 65% similarity with SEQ ID NO: 81	1-25 (SEQ ID NO: 35 & 79, 37 & 81)

Supplemental Box
(To be used when the space in any of Boxes I to VIII is not sufficient)

Continuation of Box No: II

The international application does not comply with the requirements of unity of invention because it does not relate to one invention or to a group of inventions so linked as to form a single general inventive concept. The fundamental test for unity of invention is specified in Rule 13.2 of the Regulations under the PCT.

"Where a group of inventions is claimed in one and the same international application, the requirement of unity of invention referred to in Rule 13.1 shall be fulfilled only where there is a technical relationship among those inventions involving one or more of the same or corresponding special technical features. The expression "special technical feature" shall mean those technical features that define a contribution which each of the claimed inventions, considered as a whole, make over the prior art."

In the case of the present application, the problem addressed by the application is the need in the art for materials useful in the modification of fructan and tannin content and composition in plants. The solution provided by the applicant is to provide enzymes involved in the fructan, cellulose, starch and/or tannin biosynthetic pathways isolated from forage grass tissues. Specifically, the solutions provided are in the form of 44 specific enzymes from ryegrass or fescue species and the nucleic acids or fragments coding for these enzymes. These 44 specific polypeptides fall within general groupings dependent upon which pathway they appear in (Table 1 pages 17-21). Such groupings do not confer a "special technical feature" in terms of their function.

The protein groups do share the feature of being from the plant species *Lolium* (ryegrass) or *Festuca* (fescue). However the species of origin can only constitute a special technical feature if the species or origin makes a contribution over the prior art. There is nothing in the application to indicate that isolation of peptides from fescue or ryegrass is inventive. It was known that enzymes belonging to these families would be present in ryegrass and fescue (by analogy with other plant species). The presence of these enzymes in other plant species is known in the prior art.

Therefore, none of the enzymes have any functional feature that can be seen as a "special technical feature" in common. Furthermore, none of the sequences claimed appear to have any significant homology to one another that would provide for a "special technical feature" based upon structure. Finally, none of the sequences claimed can be searched without requiring significant extra effort.

Therefore, this application is directed towards 44 separate inventions. As a service to the Applicant the ISA has searched ten separate inventions for the one fee. The Applicant selected ten sequences to be searched. The ten selected nucleotide sequences and their corresponding protein sequences that were searched are:

SEQ ID NO: 4 and 48

EQ ID NO: 12 and 56

SEQ ID NO: 15 and 59

SEQ ID NO: 17 and 61

SEQ ID NO: 20 and 64

SEQ ID NO: 22 and 66

SEQ ID NO: 27 and 71

SEQ ID NO: 33 and 77

SEQ ID NO: 35 and 79

SEQ ID NO: 37 and 81.

This Annex lists the known "A" publication level patent family members relating to the patent documents cited in the above-mentioned international search report. The Australian Patent Office is in no way liable for these particulars which are merely given for the purpose of information.

Patent Document Cited in Search Report		Patent Family Member (To put a line under the citations tab to the first point on the next row and press F8)					
WO	200195691	AU	20008155	AU	200165676	EP	1305420
WO	200231130	AU	20000673	AU	200195256		
US	2001005133	EP	1083408	JP	2001082915	US	6304076
		US	2002000129	EP	1225426	JP	2002340611
		EP	1134567	JP	2001304984		
EP	1033405		NONE				
WO	200216655	AU	200186811	CA	2420555	EP	131867
US	2002042930	AU	200118335	BR	200100470	CN	1344799
		FR	2806741				
US	6476212	NONE					
WO	2003000905	WO	2003000897	WO	2003000904	WO	2003000906
		WO	2003007699	WO	2003008540	US	2003135888
		WO	2003027249				
WO	9957285	AU	37880/99	BR	9910343	CA	2326382
		EP	1076709	US	6323015	US	2002090704
WO	9953068	AU	34748/99	EP	1070130		
WO	200164890	AU	200141622	US	2002004940	US	2003140369
WO	200220548	AU	200188741	CA	2421911	US	2002174452
WO	2002086146	NONE					

END OF ANNEX